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5.1.6	Compugen
version	- 2004
GenCore	(c) 1993
	Copyright

OM nucleic - nucleic search, using sw model

August on:

Run

6, 2004, 08:18:49; Search time 700.638 Seconds (without alignments) 7148.662 Million cell updates/sec

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> US-09-855-340A-1 1179 1 gtgtggatcgagaagaacgg......tgttggccgacgcagcatga 1179 Title: Perfect score:

Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 seqs, 2124099041 residues Searched:

6747726

seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_29Jan04:\* : geneseqn1980s:\* : geneseqn1990s:\* Database

genesequ2000s:\*
genesequ2001as:\*
genesequ2001bs:\*
genesequ2002as:\*
genesequ2003as:\* geneseqn2003cs:\* 5: 7:: 10: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:\*

SUMMARIES		Description	1 Aad25931 Micromono	Aas08694		Ada71938	Aad21926 M. rc	Aad21912 Mic	Aad17185	Aad17186	Aax53491	Aax53491	Ada71938	Aa161190	Aa161224	Aat93095	Aav25925	Aa140781	Aav47574	Aad40301	Aas96038	7 Abk81747 Leishmani	) Aaf88540 L. major	7 Adb78797 Leishmani	
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## ALIGNMENTS

Micromonospora carbonacea pMLP1 integrase DNA. BP. AAD25931 standard; DNA; 1179 (first entry) 26-MAR-2002 AAD25931; AAD25931 

Integrase; int; excisionase; xis; integrase attachment site; pMLP1; site-specific integration; hybrid antibiotic; metabolic product; secondary metabolic pathway; ds.

Micromonospora carbonacea.

WO200187936-A2.

22-NOV-2001

15-MAY-2001; 2001WO-US015760.

17-MAY-2000; 2000US-0204670P.

(SCHE ) SCHERING CORP

Horan AC; Hosted TJ,

WPI; 2002-082983/11.

Novel polynucleotides encoding integrase, excisionase and an integrase attachment site isolated from a lysogenic phage pMLP1, useful for transforming an actinomycete.

Claim 5; Page 32; 34pp; English.

The present invention relates to novel polymucleotides encoding integrase (int) and excisionase (xis) and an integrase attachment site (attp) which are isolated from pMLPI, a bacteriophage (lysogenic phage) isolated from Micromonospora carbonacea var. africana. Polymucleotides of the invention are useful for transforming an actinomycete with a vector. They are also useful for creating vectors for site-specific integration into host chromosomes. The integrating vectors are used to express actinomycete genes, manipulate secondary metabolic pathways and create new metabolic products such as hybrid antiblotics. The present sequence is pMLP1 integrase DNA from Micromonospora carbonacea

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961 GCGATCCTGATTTCTGCCGGGCGTCCGCTGTCGGCGATCTCCCGCCGCCTCGGTCACTCG 1020
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P-PSDB; AAU04900, AAU04912.
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                                             Query Match 100.0%; Score 1179; DB 6; Length 1179; Best Local Similarity 100.0%; Pred. No. 6.2e-207; Matches 1179; Conservative 0; Mismatches 0; Indels 0;
                 Sequence 1179 BP; 214 A; 370 C; 410 G; 185 T; 0 U; 0 Other;
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1081 CTCGCGGCGATCGAGGAGGCGATGGCCGCGTCCGGGCTGAGGACCTGGAGGCGGAACTC 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid molecules encoding everninomicin pathway gene products, useful for improving yields of everninomicin, to produce new everninomicin and as probes to identify homologous sequences.
1021 TCGATCGCGGTCACGGATCTGCTGTACGGGCACCTGCGTGAGGAGGTCGACGAGGGGGATC
                 1021 TCGATCGCGGTCACGGATCTGCTGTACGGGCACCTGCGTGAGGAGGTCGACGAGGAGTC
                                                                                                                                                                                                                                                                                                                                                              Everninomicin; antibiotic; bottle-neck gene; orthomicin; fermentation;
                                                          1081 CTCGCGGCGATCGAGGAGCGATGGCCGGCGTCCGGGCTGAGGAGGAGCTGGAGGCGGAACTC
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/note= "Att/B/AttP region of integrase action"
27114. 2715
                                                                                                                                        1141) GACGAGCAGCAGCACGACGCACGCAGCATGA 1179
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/note≈ "Site of integrase activity"
                                                                                                                                                                                                                                                                                                                                 Micromonospora DNA encoding integrase enzymes.
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/product= "Integrase #1"
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2570. .2799
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ce everninomicin pathway gene (a bottle-neck gene) into an actinomycete of the genus Micromonospora. The DNA encoding the biosynthetic proteins is useful for synthesising novel everninomicin-leated compounds, arising from modifications of the DNA sequence designed to change glycosyl and modifications of the DNA sequence designed to change glycosyl and conditional or mutant everninomicin, for expressing functional or mutant everninomicin biosynthetic enzyme for expressing functional or mutant everninomicin biosynthetic enzyme for other secondary metabolic products, improving the yield of everninomicins and to produce novel everninomicins and also as a hybridisation probe to identify homologous sequences. The encoded polypeptides are useful for combinatorial blosynthesis to generate libraries of orthomycins, e.g. everninomicin analogues/homologues and drug discovery. The DNA encoding the integrase allows for increasing a given gene dosage. The integrate to premanently integrate copies of a heterologous gene of choice into chromosomes of different hosts and to integrate genes which increase the yield of known products or to generate novel products or coff control antibiotics or other novel secondary metabolites. The vector can also be used to integrate antibiotic to the strain is to carry out bioconversions with compounds to which the strain is commanly sensitive and is thus useful in fermentation processes involving e.g. Streptomyces antibioticus. (Updated on 11-SEP-2003 to standardise OS
          $$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$
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6 Other 0 11 Ė Sequence 4388 BP; 714 A; 1468 C; 1506 G; 694

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<pre>ce 4388 BP; 714 A; 1468 C; 1506 G; 694 T; 0 U; 6 Other; th</pre>	н •	94 GIGIGGATCGAGAAGAACGGGCCCGTCTACCGCATTCGGGACCTCGTTCGCGGTAAAAG 61 GTCACCATTCACACCGGTTATCCGACGAGAACAGCGAGGAGAAAGAA		121 CGTGCGGAGCAGTTGCAGGGCAACGCGCTCATGCCGCGCGGCGGTCAGATTACCCTCGCC	.4 CGTGCGGAGCAGTTGCAGGGCAACGCGCTCATGCCGCGCGGCGGCGGTATTACCCTCGCC		4 GATTICGTGGGGGGAGTGGTGGCCGAGCTACGAAAAGACGCTGAAACGACCGCCGTGAAC	241 TCGGAGGCAACCGGATCCGCAACCACCTCCTGCCCATACTCGGCCATCTCACCTTGAC	4 TCGGAGGGCAACCGGAACCACCTCCTCCCCATACTCGGCCATCTCACCTTGAC	1 GAGCTGGACGGGCAGGTCACCCAGCAGTCAACGACGACGTGGAGGCGGCGTCGGCCCG	cH.	1 TGGCCGGAGTCCACGCGGGGTCGTCGGAAGCCGCTGGCTAGCAACTGC	4 TGGCCGGAGTCCACGCGGGGTCGTCCGAAGCCGCTGGCGAAGCGAAGACGAACTCAGCAACTGC	1 CACGGCCTGCTGCACACGATCTGCGGCGATCGCGGCGAAACGGATCAGGCTCAAC	4 CACGGCCTGCTGCACACGATCTGCGCGCGCGGCGGTCGCGGCGAAACGGATCAGGCTCAAC	1 CCGTGCTCTTCGACGACGATGCTGCCCCGGCGAGCCCGAAAGAGATGAAGTTCCTGAGCGAC	4 CCGTGCTCTTCGACGATGCTGCCCCGGCGCGAGAGCCGAAAGAGAGTTCCTGAGCGAC	CCGGAGATCGGTCGCCTTATCACGCCTTCCGCCGCACTGGCGACGCTCGTCGTGTGTGT	4 CCGGAGATCGGTCGGCTTATCACGGCGCTTCCGCCGCACCGCGCGCCGCTCGTCTTTTTTCACGGCGCTTCGCCGCCGCACCGCGACGCCTCGTCGTCGTG	CTGGTGGCGACCGGTCTGAGGTGGGGTGAGGCGATCGG	CTGGTGGCGACCGGTCTGAGGTGGGGTGAGGCGATCGGCCTGCGCGCCCGGCCGG
Ouery Match Best Local Sim Matches 1179;			1454	12	151	181	157	24	1634	301	169,	361	1754	421	1814	481	1874	541	193	601	1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1227 CGCTG-----AGGACGACGACGAGATCCGCATGCTCACCCACGCCGAGTTCGACCGGC 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1340 TGCGGTGGGGTGAGGTATCGGCGCTGCAGGCATGTGGATTTGGAGACGTCCACGA 1399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1508 GGCTG------GACTTGTCGAACGAGTTGTTTTCGTCAATACCGATG 1549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTCTGCCGGGCGTCCGCTGTCGGCGATCTCCCGCCGCCTCGGTCACTCGATCGCGG 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1670 TAACGGGGGACACCGGTGACGATTGTGTCTCGCCAGCTGGGTCATGAGTCGATTCAGA 1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spp., Vibrio spp., Shigella spp., Listeria spp., Streptococcus spp., Lactobacillus spp., Corynebacterium spp., and Streptomyces spp. The recombinant mycobacterium is used as a vaccine. Transformation efficiency using this integration system is higher than that of prior art DNA integration using double homologous recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   919
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                                                                                     The invention relates to the integration of a DNA fragment into a specific site of the Mycobacterium genome, using the integrative functions of a bacteriophage. A genetic system for integrating the DNA comprises: (a) DNA containing IF of a bacteriophage linked to the DNA to be expressed under control of a promoter; or (b) an integrative plasmid carrying the phage attachment site (atte) and the DNA to be expressed under control of a promoter, and a helper plasmid encoding an integrase.

The system can be adapted for other bacteria such as E. coli, Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257 TCGGCAACCACCTCCTGCCCATACTCGGCCATCTCACCCTTGACGAGCTGGACGGCAGG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCACCCCAGCAGTGGGTCAACGACCTGGAGGCGGCGTCGGCCCGTGGCCGGAGTCCACGC 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGGTCGTCGGAAGCCGCTGGCAGCGAAGACGATCAGCAACTGCCACGGCCTGCTGCACA 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1167 decencidade de maintentante de mais de descrita de decencia de descrita de decencia de descrita d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                737 AGTICGCCGAAGACCGCGAAGGGCCGGCGCCACGGTCACTTTCACCACGAAAGTCGCTCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 61.6; DB 2; Length 2404;
Pred. No. 0.022;
0; Mismatches 364; Indels 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2404 BP; 437 A; 714 C; 791 G; 462 T; 0 U; 0 Other;
Example 1; Fig 3; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 391; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1110
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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to the present of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is bacterial, fungal or viral infection. The present sequence to a plant to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 TCGTCGGAAGCCGCTGGCAGCGAAGACGATCAGCAACTGCCACGGCCTGCTGCACGCAT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 GAGCTACGAAAGACGCTGAAACCGACCGCCGTGAACTCGGAGGGCAACCGGATCCGCAA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 CCACCTCCTGCCCATACTCGGCCATCTCACCCTTGACGAGGTGGACGGGCAGGTCACCCA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 GCAGTGGGTCAAC---GACCTGGAGGCCGGCGTCGGCCCGTGGCCGGAGTCCACGCGGGG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           653 GARSMWYSKYSCSAKCCKKTRYMTSSYMSTGMYGMYSSYKSMSWTSKMSYMGKMTCTMYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           593 SMKGSTRRSKMGRWSGMSRMYMRWWKKMRKKYMRYMKWKCTWRRCMCYRWGYTMYTTSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                      Plant; bacterial infection; fungal infection; viral infection; rice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hou Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7; Length 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glazebrook J, Goff SA, Ho
Whitham S, Xie Z, Zhu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65; Conservative 277; Mismatches 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 60.4; DB 7
Pred. No. 0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 5263; 899pp; English.
1031 TCACGGATCTGCTGTACGGGCACCTG 1056
                                1730 TCACGGTGGACACGTACACGGATGTG 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                   BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cooper B,
S, Tao Y,
                                                                                                                 ADA71938 standard; DNA; 2000
                                                                                                                                                                                                                                                                                                                                                                                                            22-JUN-2001; 2001WO-IB001105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                     Rice gene, SEQ ID 5263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W, Co
7, Quan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-175290/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene expression
                                                                                                                                                                                                                                                                                                         Oryza sativa.
                                                                                                                                                                                    20-NOV-2003
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to create replicating, Escherichia coli-actinomycete shuttle, integrating and intermycelial and intramycelial conjugation vectors for use in actinomycetes. The present sequence is M. rosaria pMR2 plasmid site specific integrase gene, int. This sequence is involved in pMR2 plasmid integration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        794 ACGICGIALCCGCCIGCACCICACCICA CAGILCGCAAGGALCGCCIGILCG 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGCGCCCGAAAGGCGGGATGGTAAGGACGCGCAATTTCCGGCGGATCTGGGTCAAGGCGT 904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                965 TCCIGATITCTGCCGGGCGTCCGCTGTCGGCGATCTCCCGCCGCCTCGGTCACTCGTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCGCGGTCACGGATCTGCTGTACGGGCACCTGCGTGAGGAGGTCGACGAGGGGATCCTCG
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                                                                                                                                                                                                                                           Length 1161;
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/*tag= a
//note= "pMR2 plasmid attachment site encoding
p"
                                                                                                                                                                          Sequence 1161 BP; 188 A; 398 C; 387 G; 188 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                         299;
                                                                                                                                                                                                                                      DB 6;
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Pred. No. 0.19;
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                                                                                                                                                                                                                          Query Match
Best Local Similarity 46.2
Matches 262; Conservative
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tic; ds.
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                                                                            CTGCGGCGCGATCGCGGCGAAACGGATCAGGCTCAACCCGTGCTCTTCGACGATGCT
                                                                                                              CACGGCGCTTCCGCCGCACTGGCGACCGCTCGTCATGCTGCTGGTGGCGACCGGTCTGAG
                                                                                                                                                                                                                                                                                                                                SMMRTAGKWRAMSRWCRSYSWYKWYKKWWKKSYYMSYGWARSSGTWSRSAAKRTYKGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; vector construction; secondary metabolic pathway;
int gene; site-specific integrase; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M. rosaria pMR2 plasmid site-specific integrase gene, int
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAR-2001; 2001WO-US010321.
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AAD21926 RESULT

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Claim 20; Page 26-29; 34pp; English.

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New genes isolated from Micromonospora rosaria plasmid pMR2, useful in constructing vectors for studying and expressing genes, or in manipulating secondary metabolic pathways in actinomycetes.
                                                                                                            note = "Replication regulatory protein encoding gene,
                                                                  note = "Regulatory protein encoding gene, korR'
         *tag= b
note= "DNA replication origin encoding gene"
462. .3286
                                                                                                                                                                                                                             %tag≈ g
'*tag≈ g'
'note≈ "Intermycelial transfer gene, ORF101"
                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Intermycelial transfer gene, ORF233"
                                                                                                                                                                                                                                                                                                                                *tag= i
note= "Intermycelial transfer gene, ORF63"
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note≈ "Intermycelial transfer gene, ORF89"
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note= "Intermycelial transfer gene, ORF52"
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*tag≈ e
note≈ "Intramycelial transfer gene, traB"
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                                                                                                                                                                                                                name= "Shine-Dalgarno sequence"
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/standard name= "Shine-Dalgarno sequence"
9846. .10055
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/note= "rep gene"
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10703 --ACCGAACACACATCACCGTCCGCAAAGCCAGGGTCGAACCGCTGCACGACAGGGGGA 10760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10821 ACGICGITACCCGIGAICCGCCTGCACCTCGACGAGTTCGCCGGGAAGGATCGCCTGTTCG 10880
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                                                                                                           The invention relates to new genes isolated from Micromonospora rosaria plasmid pMR2, and proteins encoded by such genes. The isolated genes of of the invention are useful in the construction of vectors, which can be used in the study and expression of genes, in manipulating secondary metabolic pathways in actinomycetes and in creating new metabolic products such as hybrid antibiotics. The isolated genes can also be used to create replicating, Escherichia coli-actinomycete shuttle, integrating and intermycelial and intramycelial conjugation vectors for use in actinomycetes. The present sequence is M. rosaria pMR2 plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         545 AGAICGGTCGGCTTAICACGGCGCTTCCGCCGCACTGGCGACCGCTCGTCATGCTGCTGG 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         665 TCGCCGCGCGCCCCGGCTGACCGTCGTCGAGCAGCTCCAGGAGCTGGCCAGCACGGGAG 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               845 CCGCGCCGAAAGGCCGGATGGTAAGGACGCGCAATTTCCCGGCGGATCTGGGTCAAGGCCGT 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    905 GCGAGGAAGCCGGGCTTCCGGGCTTACGCATTCACGATCTGCGGCACACTCACGCGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCTCGTCTTCCAGTCGCCGAAGACCGCGAAGGGCCGGCGCACGACGTTTCACCACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11188 BP; 1749 A; 4113 C; 3447 G; 1879 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.8%; Score 56.6; DB 6; Length 11188;
46.2%; Pred. No. 0.18;
tive 0; Mismatches 299; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces noursei nys2 DNA of nystatin PKS gene cluster.
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ID AAD17185 standard; DNA; 27541 BP
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Matches 262; Conservative
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1591 GGCCGCCCGGACCGCGACGGCGATGGGCCGCGATCTGCGGTCCGCCGCTCTTCCGCCGCAT 4532
                                                                                         4531 ccredactricicacacadedahicaecagricaecacacacacacacatacaeacaeaca 4472
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                                                  CTGCCACGCCTGCTGCACACGATCTGCGGCGGCGATCGCGGCGAAACGGATCAGGCT
                                                                                                                                                                     4471 GGTGAACGACGTGCAGCAGGTGCAGAACCTCGCCCAGACGGGTTCGGCATCGTCGTCTG
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                                                                                                                                                                                                               CGACCCGGAGATCGGTCGGCTTATCACGGCGCTTCCGCCGCACTGG----CGACCGCTCGT
                                                                                                                                                                                                                                                                                          594 CATGCTGCTGGTGGCGACCGGTCTGAGGTGGGGTGAGGCGATCGGCCTGCGCCCGGCCG
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84792. 51099
**tag= b
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/product= "NysK protein"
57503. .58687
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1155. .57355
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AAD17186/c
ID AAD17186 standard; DNA; 125401 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nystatin polyketide synthase polynucleotides and polypeptides, useful as antibiotics and antifungals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to the cloning and sequencing of the gene cluster encoding a modular type I polyketide synthase (PKS) enzyme involved in the biosynthesis of the macrolide antibiotic nystatin. The nystatin PKS is useful as antifungal antibiotics. The present sequence a Streptomyces noursei nys2 DNA of nystatin PKS gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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14.8%; Pred. No. 0.25;
Ive 0; Mismatches 417; Indels 10;
                                                                                                                      /note= "CDS does not include start codon"
complement(1275. .3092)
                                                                                                                                                                                                                    *tag= c
/note= "CDS does not include start codon"
                                                                                                                                                                                                                                                                                                                                                                                   product= "NysI partial protein"
note= "CDS does not include stop codon"
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P-PSDB; AAE10138, AAE10139, AAE10140, AAE10141, AAE10142.
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Sletta H, Gulliksen O;
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3F STIFTELSEN IND TEK FORSK.
                                                                                                                                                                                                                                                          /product="NysH protein"
5122. .6156
/*tag= d //product="NysD3 protein"
6338. .27541
                                                                                                   "NysF protein"
                                                                                                                                                                                /product= "NysG protein"
complement(3070, .4824)
                                                               complement (454. .1191)
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                                          Location/Qualifiers
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10-APR-2000; 2000GB-00008786.
14-APR-2000; 2000GB-00009387.
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Best Local Similarity 44.8%;
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DZIECLEWSKA H.
ZOTCHEV S B.
SEKUROVA O N.
FJAERVIK E.
STROM A R.
VALLA S.
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  Streptomyces noursei
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Valla S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            828 TGACGAGGTCGTGTTCACCGCGCCGAAAGGCGGGATGGTAAGGACGCGCAATTTCCGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGCCACGGCCTGCTGCACACGATCTGCGGCGCGCGATCGCGGCGAAACGGATCAGGCT 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 125401 BP; 15664 A; 49692 C; 42871 G; 17174 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.7%; Score 55.8; DB 4; Length 125401;
44.8%; Pred. No. 0.24;
live 0; Mismatches 417; Indels 10; Gaps
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AAE10149, AAE10150
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                                                                                                                                                                                                                                          /note= "CDS does not include start codon"
complement (59045. .60241)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note≈ "CDS does not include start codon"
complement(60238. .61296)
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etta H, Gulliksen O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag= 9
product= "NysD2 complete protein"
20628. .121308
*tag= h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag≈ h
/product= "NysR4 (long) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
                                                           /product= "NysL protein"
complement(58786. .58980)
                                                                                                                                                                                                    "NysM protein"
                                                                                                                                                                                                                                                                                                                                                                                                             "NysN protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sletta H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as antibiotics and antifungals.
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10-APR-2000; 2000GB-00008786.
14-APR-2000; 2000GB-00009387.
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Valla S, Ellingsen TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 44.8
Matches 346; Conservative
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DZIEGLEWSKA H.
ZOTCHEW S B.
SEKUROVA O N.
FJAERVIK E.
                                                                                                                                                                   *tag≈
          /*tag≈
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALPHARMA AS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SINVENT AS
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(ZOTC/)
(SEKU/)
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(STRO/)
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98US-00093972.
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directed against at least 2 mRNAs selected from target genes, coding and
non-coding regions of RNAs corresponding to target genes, gene initiation
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
end and the juxta-section between coding and non-coding regions and all
segments of RNAs encoding proteins associated with one or more diseases,
conditions or mixtures. The antisense oligonucleotides may be derived
from sequences AAX55272-74. These multiple target oligonucleotides
conditionally AAX5180-271) can be used for the antisense treatment of
diseases and conditions. Typical diseases and conditions are those
associated with impaired respiration and inflammation, including lung
classases, pulmonary vasconstriction, inflammation, respiratory
classases, syndrome, pain, cystic fibrosis, pulmonary hypertension,
colon cancer, breast cancer, lung cancer, pancreatic cancer,
colon cancer, breast cancer, lung cancer, melanoma, hepatic metastases,
colon cancer, breast cancer, lung cancer, melanoma, hepatic metastases,
colon cancer, breast cancer, lung cancer, melanoma, hepatic metastasized
colon cancer settinoma, kidney cancer, melanoma, hepatic metastasized
colon cancer breast and prostate cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 0 U; 21427 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 CGTGAACTCGGAGGGCAACCGGATCCGCAACCACCTCCTGCCCATACTCGGCCATCTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 CCTTGACGAGCTGGACGGCCAGGTCACCCAGCAGGTCAACGACCTGGAGGCCGGCGT
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                                                                                                                        pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.7%; Score 55.2; DB 2; Length 114955; 31.6%; Pred. No. 0.32; ive 98; Mismatches 538; Indels 9;
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                                                                                                                     antisense oligonucleotides used in treatment of,
                                                                                                                                                               Disclosure; Page 37; 120pp; English
 98US-00093972.
                            (UYEC-) UNIV EAST CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                        WPI; 1999-229400/19
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.1998;
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                                                          Nyce JW
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104603 INSGGCGGCGCCCVGCCVGCGGNNHNNNSCGGCGCGCGCCCVGCCGCNNHNN 104544
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                                                                                                                                                                                                                                                                                                                                                                                               104663 GINHININSCGGCGCGCCCVGCGCCVGCGGNNHININSGCGGCGCGCCCVGGCCVGCGGNHHN 104604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1072
                                                                                                                                                                                                                       104723 VGGCCVGCGGNNHNNNSGCGCGCCCVGGCCVGCGGNNHNNNSGGCGCCCCVGCCCVGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCACGCGGCGATCCTGATTTCTGCCGGGCGTCCGCTGTCGGCGATCTCCCGCCGCCTCG
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                                                                                                                                            CTACTGCTTACGCCACTCATCGCCGGAAAGAAAGTGACG
                                                                                                                                                                                                                                                                                                               AGGICGIGITCACCGCGCCGAAAGGCGGGATGGTAAGGACGCGCAATTTCCGGCGGATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human adenosine Al receptor antisense oligonucleotide fragment.
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958 GCGGCGATCCTGATTTCTGCCGGGCGTCCGCTGTCGGCGATCTCCCGCCGCCGCCTCGGTCAC 1017

104705 GCSNNNDNNCCGCBGGGCCGCGSNNNDNNCCGCBGGGCGCGCSNNNDNNCCGC 104764 104885 CCSNNNDNNCGCBGGCCBGGCGGCGCGCCGC----CGGCCGGGCCGSNNNDNNGCBGGCCBG 104940 105001 NDNNBGGCCBGGGCGCGCCGGCCGGCCGSNNNDNNGGCCBGGGCGCGCGCGCGCGCCGCCGCCGCC 104645 BGGGCGCCGCCGSNNNDNNCCGCBGGCCBGGCGCGCSNNNDNNCCGCBGGCCBGGCGC 104704 104765 BGGCCBGGGCGSNNNDNNCCGCBGGCCBGGCSNNNDNNCCGCBGGCCBGGGSNNNDNNC 104824 104825 CGCBGGCCBGGSNNNDNNCCGCBGGCCBGSNNNDNNCCGCBGGCCBSNNNDNNCCGCBGG 104884 The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and anno-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX55272-74. These multiple target oligonucleotides (specifically AAX55180-271) can be used for the antisense treatment of 717 360 GTGGCCGGA--GTCCACGCGGGGTCGTCGGAAGCCGCTGGCAGCGAAGACGATCAGCAAÇ 417 477 177 AACCCGTGCTCTTCGACGATGCTGCCCCGGCGCGGAGAGAAAGAGATGAAGTTCCTGAGC 537 pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (GOPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, mananceatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as 538 GACCCGGAGATCGGTCGGCTTATCACGGCGCTTCCGCCGCGCACTGGCGACCGCTCGTCATG 597 Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 0 U; 21427 Other; Datocellular carcinoma, kidney cancer, melanoma, hepatic metastases, a lass all types of cancers which may metastasize or have metastasized the lungs, including breast and prostate cancer diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, TGCCACGGCCTGCTGCACACATCTGCGGCGCGCGATCGCGGCGAACGGATCAGGCTC 658 GACCTGCTCGCCGCGCGCGCCCCGGCTGACCGTCGAGGAGCAGCTCCAGGAGCTGGCCAGC 718 ACGGGAGAGCTCGTCTTCCAGTCGCCGAAGACCGCGAAGGGCCGGCGCACGGTCAGTTTC 300 CGAGCTGGACGGGCAGGTCACCCAGCAGTGGGTCAACGACCTGGAGGCCGGCGTCGGCCC 6; Gaps 4.7%; Score 55; DB 2; Length 114955; 30.7%; Pred. No. 0.34; ive 80; Mismatches 477; Indels 6. Disclosure; Page 37; 120pp; English. Best Local Similarity 30.79 Matches 249; Conservative 418 Query Match  $\overset{\mathsf{A}}{\times}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}$ 임 g Š ઠે  $\delta$ g Š 임 Š qq Š g ð qq ò g

105061 GGGCCGSNNNDNNGCCBGGCGCGCGCCGCGGGCCGSNNNDNNCCBGGGCGCGCGCGC 105120 105121 CGGCCGGGCCGSNNNDNNCBGGCGCGCCGCCGGCCGGCCGSNNNDNNBGGCGCGCGC 105180 .05181 CCGGCCGGGCCGSNNNDNNGGGCGCGCCGCCGGCCGGGCGGSNNNDNNGGCGCGCCGCCG 105240 957 838 GTGTTCACCGCGCCGAAAGGCGGGATGGTAAGGACGCGCAATTTCCGGCGGATCTGGGTC 897 898 AAGGCGTGCGAGGAAGCCGGGGCTTCCGGGCTTAACGCATTCACGATCTGCGGCACACTCAC

105241 GCCGGGCCGSNNNDNNGCGCGCCGCCGGCCGGGCCGSNNNDNNCGCGCCGCCGCCGGCCGGGC 105300

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105361 GGCGGGCCGGGCCGSNNNDNNCCGCCGGCCGGNNNDNNCGCCGGCCGGCCGGSNN 105420 1018 TCGTCGATCGCGGTCACGGATCTGCTGTACGGGCACCTGCGTGAGGAGGTCGACGAGGGG 1077 involved in plant resistance or response to pathogenic infection. Mi comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention. 2 2 231 CGCCGTGAACTCGGAGGGCAACCGGATCCGCAACCACCTCCTGCCCATACTCGGCCATCT 290 291 CACCCTTGACGAGCTGGACGGGCAGGTCACCCAGCAGTGGGTCAACGACCTGGAGGCCGG 350 Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant .. .. .. .. h Similarity 10.5%; Pred. No. 0.77; 79; Conservative 353; Mismatches 311; Indels 11; Gaps Plant; bacterial infection; fungal infection; viral infection; rice; present invention relates to a method (MI) for identifying genes Hou Y; F, Zou G; Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other; Goff SA, Hora Z. Zhu T, Glazebrook J, Goff Whitham S, Xie Z, 105421 NDNNGCCGGCCGGSNNNDNNCCGGCCGG 105452 1078 ATCCTCGCGGCGATCGAGGAGGCGATGGCCGG 1109 Claim 27; SEQ ID NO 5263; 899pp; English. ..... (SYGN ) SYNGENTA PARTICIPATIONS AG. ADA71938 standard; DNA; 2000 BP. 22-JUN-2001; 2001WO-IB001105. Cooper B, 3, Tao Y, 22-JUN-2001; 2001WO-IB001105. (first entry) Rice gene, SEQ ID 5263. <u>..</u> ... ... Chang H, Chen W, Co Katagiri F, Quan S, WPI; 2003-175290/17. WO2003000898-A1. gene expression Oryza sativa. 20-NOV-2003 03-JAN-2003. 79; ADA71938; gene; ds. Query Match Local Matches RESULT 11 Op ò 음 g ઠે ò ò

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                                                                                                                                                                                                                   GCTGGCCAGCACGGGAGGCTCGTCTTCCA-----GTCGCCGAAGACCGCGAAGGGCCG 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maytansinoid; ansamitocin; antitumour; O-methyltransferase; enzyme; gene;
                            119 YRRCARSGRMAGGSGRMMGGKSRMSYWMWCYARGGSCKRKKKSKGGSWGKTCRRGARGGS
                                                CAGCAACTGCCACGGCCTGCTGCACACGATCTGCGGCGCGGCGATCGCGGCGAAACGGAT
                                                                                 CAGGCTCAACCCGTGCTCTTCGACGATGCTGCCCCGGCGCGCGAGCCGAAAGAAGATT
                CGTCGGCCCGTGGCCGGAGTCCACGCGGGGTCGTCGGAAGCCGCTGGCAGCGAAGACGAT
                                                           GWSSGAKYKSGSMSKRMWMSSCGRSGGRRSAYSRYYGTSRKYGTYKKMTYYSASRCMRA
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The invention relates to maytansinoid produced by bacterial host cell transformed with expression vector comprising open reading frame from ansamitocin gene cluster I of Actinosymmema pretriosum. Maytansinoid is useful as a potent antitumour agent. The present sequence is A. pretiosum ansamitocin gene cluster I O-methyltransferase gene
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                                                                                                                                                                                            Novel maytansinoid produced by bacterial host cell transformed with expression vector comprising open reading frame from ansanitocin gene cluster I of Actinosymbem preticeum, useful as antitumor agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 504 BP; 57 A; 192 C; 190 G; 65 T; 0 U; 0 Other;
                                                                                                                                                                                  maytansinoid produced by bacterial host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maytansinoid; ansamitocin; antitumour; gene;
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Best Local Similarity 46.6%;
Matches, 170; Conservative (
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'product= "protein with 6 membrane-spanning domains"
note= "gene C (specifically claimed)"
                                                                                                                                                                                                                                                         product= "ATP-binding component of ABC transporter"
|note= "gene D (specifically claimed)"
|533. ,7183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "acyl carrier protein used by the PKS"
/note= "gene N (specifically claimed)"
complement(16453. .16935)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product = "cyclase/dehydrase related to act VII"
/note= "gene Q (specifically claimed)"
18895. 19839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      related to actIV" claimed) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "translationally coupled to gene I"
/note= "gene H (specifically claimed)"
complement(10618. .11628)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product= "ketoreductase related to actIII"
note= "gene P (specifically claimed)"
                                                                                                                                                                                                                                                                                                                                  product= "unknown non-membrane protein"
note= "gene E (specifically claimed)"
1344. .8897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product= "PKS ketoacylsynthase subunit"
note = "gene L (specifically claimed)"
4767. .16047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'product= "putative hemiketal dehydrase"
note= "gene O (specifically claimed)"
7088. .17903
/note= "gene A (specifically claimed)" 2945. .3916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "transcription activator"
/note= "gene G (specifically claimed)"
complement(10105. .10621)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product = "PKS chain length factor"
notes "gene M (specifically claimed)"
(6120. 16371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= j
/product= "acyl carrier protein"
/note= "gene J (specifically claimed)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note≈ "gene K (specifically claimed)"
[3409, .14686
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/note= "gene S (specifically claimed)"
                                                          /product= "membrane protein"
/note= "gene B (specifically claimed)'
4020. .4844
                                                                                                                                                                                                                                                                                                                                                                                                                                         'product= "putative efflux pump"
'note= "gene F (specifically claimed)'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "gene I (specifically claimed)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product= "homologue of fabH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "cyclase/dehydrase
/note= "gene R (specifically
complement(19990. .20907)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product= "acyltransferase"
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       48121 AGCTGAGCCCCAAGTGGCCCGCGATCGCCCGGCCGCCACTGGGAGCGCGCGGGCGTCGCGG 48062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18001 TCGCGGGCCGGGTCGACCTGGTGTTCGTGGACGCGGACAAGGCCGGGTACCCCCGCTACT 47942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                 The invention relates to maytansinoid produced by bacterial host cell transformed with expression vector comprising open reading frame from ansamitooin gene cluster I of Actinosymmema pretiosum. Maytansinoid is useful as a potent antitumour agent. The present sequence is A. pretiosum ansamitocin ansamitocin biosynthetic gene cluster I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 644 GCGCCGGCCGGGTCGACCTGCTCGCCGCGGCCCCGGCTGACCGTCGTCGAGCAGCAGCTCC 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      464 AACGGAICAGGCICAACCCGIGCTCTTCGACGAIGCTGCCCCGGCGCGCGAGCCGAAAGAGA 523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         704 AGGAGCTGGCCAGCACGGGAGAGCTCGTCTTCCAGTCGCCGAAGACCGCGAAGGCCCGGC 763
                                                                                                                Novel maytansinoid produced by bacterial host cell transformed with expression vector comprising open reading frame from ansamitocin gene cluster I of Actinosynnema pretiosum, useful as antitumor agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47881 TCTCCGGCCGGGTCGCCGGACCCCGGCGGTGGACCCCGACACCGAGGGCGTCCGGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Frenclicin; antibiotic; feed additive; anticoccidial; coccidiostatic; efflux pump; butyrate starter synthase; polyketide synthase; PKS; hemiketalase; ketoreductase; cyclase; dehydrase; ketoreductase; hydroxylase; Streptomyces roseofulvus; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 82746 BP; 10231 A; 31648 C; 32359 G; 8508 T; 0 U; 0 Other;
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                                                                                                                                                                                                          Claim 7; Page 105-152; 160pp; English.
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636. .2948
/*tag= a
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                          Yu T,
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                          Floss HG,
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transl_except= (pos:4020, .4022,aa:Met)
'note= "encodes protein given in AAW55802"
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note= "encodes protein given in AAW55800"
945. .3916
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/transl except= (pos:11628. .11626,aa:Met)
/note= Tencodes protein given in AAW55808"
11809. .12066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= k
/transl_except= (pos:13209. .13207,aa:Met)
/note= "encodes protein given in AAW55810"
13409. .14686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag= b
|Transl except= (pos:2945. .2947,aa:Met)
|note="encodes protein given in AAW55801"
|020. .4844
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note= "encodes protein given in AAW55804"
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/transl_except= (pos:9164, .9166,aa:Met)
/note= "encodes protein given in AAW55806"
complement(10105, .10621)
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/transl_except= (pos:10621. .10619,aa:Met)
//note="encodes protein given in AAW55807"
complement(10618. .11628)
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complement(16453, .16935)
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/note= "encodes protein given in AAW55815"
17903. .18898
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9164. .10012
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/note= "encodes protein given in AAW55811"
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note= "encodes protein given in AAW55814"
.7088. .18903
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                                                                                                                                                                                                                                                                                      Streptomyces roseofulvus frenolicin gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
636. .2948
              AAV25925 standard; cDNA; 24379 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (16453.
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7344. .8897
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                                                                                                      AAV25925;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This DNA sequence comprises the Streptomyces frenclicin gene cluster containing specifically claimed coding sequences (genes A-U) that containing specifically claimed coding sequences (genes A-U) that containing specifically claimed coding sequences (genes A-U) that caspectively encode 2 proteins (see AAM34199-219) involved in frenclicin synthesis. The genes can be divided into 5 subclusters: (1) genes A, B, C, D and F encode an efflux pump; (2) genes H, I, J and K encode butyrate container synthases; (3) genes L, M and N encode polyketide synthases (PKS) (5; (4) genes O, P, Q and R encode a keto/encyl reductase and cyclases/dehydrases; and (5) genes S and T encode a keto/encyl reductase and a hydrolase. Also claimed are vectors, host cells (especially a Streptomyces rosecfulvus), and the encoded proteins. Cells transformed using the above sequence can be cultured to proteins. Cells transformed using the above sequence can be cultured to converted to frenolicins by chemical or other methods. The frenolicins can be oxidised to frenolicins a enimal feed additives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces frenolicin gene cluster - useful for producing recombinant frenolicin antibiotics.
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P-PSDB; ARWA199, AAWA4200, AAW34201, AAW34202, AAW34203, AAW34211,
AAW34205, AAW34206, AAW34207, AAW34208, AAW34209, AAW34210, AAW34211,
AAW34212, AAW34213, AAW34214, AAW34215, AAW34216, AAW342118,
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4.5%; Score 52.8; DB 2; Length 24379;
Best Local Similarity 52.2%; Pred. No. 0.89;
Matches 117; Conservative 0; Mismatches 107; Indels 0;
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/product= "quinone-forming hydroxylase"
/note= "gene T (specifically claimed)"
complement(22505. .22179)
complement (20904. .22094)
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/product= "not specified"
/note= "gene U"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGGCACACACGCGGCGATCCTGATTTCTGCCGGGCGTCCGCTGTCGCGATCTCCCG 1004
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/*tag=_ s
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complement(20904, .22094)
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time : 705.638 secs

Search completed: August 6, 2004, 09:47:28

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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llarity 100.0%; Pred. No. 4.3e-159;
Conservative 0; Mismatches 0;
                                                            organism="Micromonospora" (mol_type="unassigned DNA" /db_xref="taxon:47853"
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Development of the Micromonospora carbonacea var. africana ATCC
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in Micromonospora spp
Microbiology (Reading, Engl.) 149 (Pt 9), 2443-2453 (2003)
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Hosted,T.J. D.T., Alexander,D.C. and Hewitt,D.D.
Hosted,T.J. D.T., Alexander,D.C. and Hewitt,D.D.
Bubmitsaion
Submitted (12-SEP-2002) New Lead Discovery, Schering-Plough
Submitted (12-SEP-2002) New Lead Discovery, Schering-Plough
Research, 2015 Galloping Hill Road, Kenliworth, NJ 07033, USA
1. 2025
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/specific_host="Micromonospora sp. ATCC 39149"
/specific_host="micromonospora"
/note="host is deposited in ATCC as Micromonospora carbonacea var. africana Waitz et al."
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LGGARLAMPRAGOLTLADFVSWFWPSYRTIKRFYANSBGORTRRHATHIDEL
LGGARLAMPRAGOLTLADFORDFRIGHTAKTISNCHGILHTIGCAALAKRIRIN
PCSSTMLPRREPKEMKFLSDPEIGRLITALPPHWRPLVMLLVATGLRWGBAIGLRAGR
LDLAARPRIVVEQLQELASTGELVFOSPKTAKRRTVSTTYVALLLITPLIAGKKS
DEVVFTAPKGGWYPTRNFIWYKACEEGLGLERTHDLATHIAAILISAGRPLSAIS
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| transl_table=11
| protein_id="cAc60078.1"
| db_xref="G1:15386337"
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Patent: WO 0151639-A 176 19-JUL-2001;
Schering Corporation (US)
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VDLLAARPRITVVEQLQELASTGELVFQSPKTAKGRTVSFTWALLLITPLIAGKKS
DEVVPFTARPRGHVRTRNFRRIWYKACEREAGLFGLR.HDLLRHTHAAILISAGRELSALE
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; Pred. No. 3.8e-159;
0; Mismatches 0;
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1925. .1986
/note="attP element"
join(1969. .1986,1991. .2010)
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Best Local Similarity 100.0%;
Matches 1179; Conservative 0
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misc_feature
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                                                                                                          AP002994 347660 bp DNA linear BCT 15-MAY-2001 Mesorhizobium loti DNA, complete genome, section 1/21.
                                                                                                                                                                                                                                                                                             Kaneko, T., Nakamura, Y., Sato, S., Asamizu, E., Kato, T., Sasamoto, S., Watanabe, A., Idesawa, K., Ishikawa, A., Kawashima, K., Kimura, T., Kishida, Y., Kiyokawa, C., Kohara, M., Matsumoto, M., Matsumo, A., Mochizuki, Y., Nakayama, S., Nakazaki, N., Shimpo, S., Sugimoto, M., Takeuchi, C., Yamada, M. and Tabata, S.
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Submitted (05-DBC-2000) Takakazu Kaneko, Kazusa DNA Research
Institute, The First Laboratory for Plant Gene Research; Yana
1532-3, Kisarazu, Chiba 292-0812, Japan
(E-mail:kaneko@kazusa.or.jp,
URL:http://www.kazusa.or.jp,
Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)
On May 11, 2001 this sequence version replaced gi:11994962.

Location/Qualifiers
                                                                                                                                                                                                                                        Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Phyllobacteriaceae, Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                        Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti DNA Res. 7 (6), 331-338 (2000) 21082930
1141 GACGAGGAGCTGACGGACGTTTGGCCGACGCAGGA 1176
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AP002994.2 GI:14021068
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Mesorhizobium loti
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                                                                                  GATTTCGTGGGGGAGTGGTCGCCGAGCTACGAAAAGACGCTGAAACCGGCCGTGAAC
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YRVPVPFHDLEDRLRALATKAGASLKSVLHAAHLKTLSMLTEEDRFFSGLVCNARPEV
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Shiba,T., Sakaki,Y., Hattori,M. and Omura,S.
Complete genome sequence and comparative analysis of the industrial
microorganism Streptomyces avermitthis
Nat. Biotechnol. 21 (5), 526-531 (2003)
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     GATCAGGCTCAACCCGTGCTCTTCGACGATGCTGCCCCGGCGCGAGCCGAAAGAGAGATGAA 527
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Streptomyces avermitilis genomic DNA, complete genome, section
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                                                                                                                                                                                                                         GTTCCTGAGCGACCCGGAGATCGGTCGGCTTATCACGCGCGCTTCCGCCGCACTGGCGACC
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Streptomyces avermitilis MA-4680
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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21477403
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AP005036.1 GI:29607295
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OOMDLEMENT (11156 ... 16285)

// OCCE="SAV3643

nrpg2 gene cluster, NRPS involved in dihydroxy-benzoyl-glycine biosynthesis"

// codon start=1

// transl table=11

// product="putative non-ribosomal peptide synthetase"

// protein\_id="BAC71355.1"

// db xref="gr125607297"

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RLVAGAGPALAGPPRAGARRVGPETPPRSDBAGPLAADPANAAYAVFTSGSTGRP

KUVVUTHAGIANNE IGMTUQUYES LELELEN BALBADIPMAATA NETSASIGKE 
KAUVVUTHAGIANNE IGMTUQUYES LELELEN BEDAAGNE IF PELVIGGGTVVILAP 
AGARED PAALIRAVADHGVTVLQVVES VILELUVEEGDMS GCGSIRILIFSAGGALHAEL 
VARLERER TGQDLE WMYTG PTECS ID TTAGVUD PALITAGE VETERER EDEGMS TUVIGEN 
GVPUTUR TGGELD MYNTG PTECS ID TTAGVUD PALITAGE VETERER EDEGMS TUVIGEN 
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/note="SAV364 nrps2 gene dluster" /codon start=1 /transI\_table=11 /product="putative MbtH-like protein" /product="putative MbtH-like protein" /product="putative MbtH-like protein" /db\_xref="G1:29607298" /transLation="MTAEQTAQQAADQPAQQAAQQSEGPVQRVVFNDEEQYSLWPAGR DLPAGWHAEGTEGSREECLARIAEVWTDMRPLSLRRHWHESSAA" /gene="arcB2" 115431 CGTGCCTGAGCGCCCTGTTTTGTCGGTGGCGAAGTCTTTGGCGTCGCCTATGCCATTGC 115372 115312 115141 115021 115260 ccaccadadaccaadrracaaaacddacadcrcrrcaacaadacdccaadrcad 115201 115261 HCAARLPEYMIPATFTALDTIPVNANGKVDRSALPAPGRTADDESHVAPSGPVZERVA EIWTELLGVQAGAHDNFFHIGGNSILAIRLISHLQQBFEIDFAVRTVFEGPTVARIAA TVEERVTAQIAALSDADLLDDAARTDTTHLTNNPALKEHQA" /KIRGYRVELGEIQAVLTAHPAVRDAVVTVHRPENGEPTLAAHVVPADAAAPLPDLAA 512 632 692 752 812 ------CGCCGGAAAGAAAGTGACGAGTCGTGTTTCACCGCCGGAAAGGCGGGAT 863 923 115371 ACCGCGCTACCGCTGCTCCTCGGCTGCGTTCACGACTCTCCGCTTCGGCGAGCT GCTGGCAGCGAAGGATCAGCAACTGCCAGGGCCTGCTGCACAGGATCTGCGGCGGG 115551 GGTGGGGGAGCCCACGGTGGTCAAGGCGTACCAACTGCTGCGGGGCCCTGATGAACACCGC 573 GOGGAACTGGCGACCGCTCGTCATGCTGGTGGCGACCGGTCTGAGGTGGGGTGAGGC 115311 GGCCGCCTCCTCGCAAGGACATCGATCTGAACGGT------CGCTTGGTTGTGCT GATCGCGGCGAAACGGATCAGGCTCAACCCGTGCTCTTCGACGATGCTGCCCCGGCGCGA GATCGGCCTGCCCGGCCCGGGTCGACCTGCTCGCCGCGCGCCCCCGGCTGACCGTCGT cecededetricandesirrectricedecreacidereaceadareaceaceae 115140 GAAGCACTACGCCGCCGATGGTCAGAAGGCCCACTGTTCGTTGGTCCACAGGGTGGGCA CGAGCAGCTCCAGGAGCTGGCCAGCACGGGAGGCTCGTCTTCCAGTCGCCGAAGACCGC GAAGGCCCGCCACGGTCAGTTTCACCACGAAAGTCGCTCTACTGCTTACGCCACTCAT GGTAAGGACGCGCAATTTCCGGCGGATCTGGGTCAAGGCGTGCGAGGAAGCCGGGCTTCC Gaps 21; DB 1; Length 300800; Query Match
5.6%; Score 65.8; DB 1; Length 300
Best Local Similarity 48.9%; Pred. No. 0.99;
Matches 280; Conservative 0; Mismatches 272; Indels 924 GGGCT---TACGCATTCACGATCTGCGGCACAC 953 complement (16629. .17633) /gene="arcB2" 453 633 753 ( 813 393 693 115200 864 CDS à 셤 ò d ò g  $\dot{\circ}$ g ò g ò d ò qq δ B δ d ò

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                            PRI 18-JAN-2002
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                                                                                                                                                                                                                                                                                                                                    Loases 1 to 125020)
Johnses, S.B., Ingersoll-Ashworth, R.G., Ross, C.A. and Margolis, R.L.
Direct Submission
Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical
Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
1. .125020
                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                           1 (bases 1 to 12502)
Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang,H.S., Ingersoll-Ashworth,R.G., Fleisher,A., Stevanin,G., Brice,A., Potter,N.T., Ross,C.A. and Margolis,R.L.
A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2 Nat. Genet. 29 (4), 377-378 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 GGATCCGCAACCTCCTGCCCATACTCGGCCATCTCACCCTTGACGAGGTGGACGGC
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/db_yred="l64"
/map="l64"3; between D168520 and WI-12410"
/mofe="isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
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                          AF429315
Homo sapiens junctophilin 3 (JPH3) gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.6%; Score 65.6; DB 9; Length 12
llarity 11.3%; Pred. No. 1.3;
Conservative 390; Mismatches 381; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_unit="ctg"
complement(<36507. .>36887)
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complement(<36507...>36887)
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complement(<36507. .36887)
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complement(35581, .35746)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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17351
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                                                                                                                                                     SSWCMGWGA----GYRRSKRSAGWGAGWRSSKGKRSTGMKRACSKKTGSYGSTGRSWKKK 17471
                                                                                                                                                                                                                                                                             17292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      967 CTGATITICIGCCGGCGTCCGCTGTCGGCGATCTCCCGCCGCCTCGGTCACTCGTCGATC 1026
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434 ACACGATCTGCGGCGGCGATCGCGGCGAAACGGATCAGGCTCAACCCGTGCTCTTCGA 493
                                                                                                                                                                                                                                                                                                                                                            673
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(bases 1 to 125020)

Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang, H.S., Ingersoll-Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, A., Potter, N.T., Ross, C.A. and Margolis, R.L.
A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2

Nat. Genet. 29 (4), 377-378 (2001)
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Holmes, S. J. Ingersoll-Ashworth, R.G., Ross, C.A. and Margolis, R.L.
Direct Submission
Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical
                                                                                                                                                                                                                                                                                                                                                                                                   17350 AGRGCYSSS-MWSTRKRRSKCYSYKSYKKGRGROKKGMGGMKRGSKYWSSMKKOKRSSWSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1027 GCGGTCACGGATCTGCTGTACGGGCACCTGCGTGAGGAGGTCGACGAGGGGATCCTCGCG
                                            17586 YCMTYYYSKSCTYKSSTCYKRGGYYWGSKTCYSAGGKSRSMYYCMMRSSKSSSWSMAR
                                                                                                                        CGATGCTGCCCCGGCGCGCGCAAAGAGATGAAGTTCCTGAGCGACCCGGGAGATCGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               674 GGCCCCCGCCTGACCGTCGAGCAGCTCCAGGAGCTGGCCAGCACGGAGAGCTCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       734 TCCAGTCGCCGAAGACCGCGAAGGCCCGCGCGCCACGGTTTCACCCACGAAAGTCGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17231 Yrrsrammignaaagcttccccantnggggaaaaggggggggskscy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 907 GAGGAAGCCGGGCTTCCCGGGCTTACGCATTCACGATCTGCGGCACACTCACGCGGCGATC
                                                                                                                                                                                                                                                                                                                                                            614 GTCTGAGGTGGGGTGAGGCGATCGGCCTGCGCCGGCCGGGTCGACCTGCTCGCCGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               847 GCGCCGAAAGGCGGGATGGTAAGGACGCGCAATTTCCGGCGGATCTGGGTCAAGGCGTGC
                                                                                                                                                                                                                                          GGCTTATCACGGCGCTTCCGCCGCACTGGCGACCGCTCGTCATGCTGCTGGTGGCGACCG
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Homo sapiens junctophilin 3 (JPH3) gene, partial cds.
AF429315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16931 KSKGGSWAKGMVWDKGSVSTDKSDKWBSRSBSKVKSKWSMSRR 16889
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17187
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/db_xref="G1:17646245."
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HGFEVLGYYWPSGATYYCGTWAQGTRHGIGLESKGKWVYKGEWTHGFKGRYGVRECAG
NGAXYEGTWSNGLQDGYGTETYSDG."
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                                                                                                                                                                                                                                                                                                                                       gene="JPH3"
note="component of the junctional complex between plasma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       486 CTCTTCGACGATGCTGCCCCGGCGCGGAGCCGAAAGAGAGATGAAGTTCCTGAGCGACCCGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       546 GATCGGTCGGCTTATCACGGCGCTTCCGCCGCACTGGCGACCGCTCGTCATGCTGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         666 CGCCGCGCCCCCCGGCTGACCGTCGTCGAGCAGCTCCAGGAGCTGGCCAGCACGGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                              /map="16q24.3; between D16S520 and WI-12410"
/note="isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
 Wolfe St., Baltimore, MD 21287, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

5.3%; Score 62.4; DB 9; Length 125020;
Best Local Similarity 12.2%; Pred. No. 3.7;
Matches 109; Conservative 387; Mismatches 392; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                         nembrane and endoplasmic reticulum
                                                                                                                                                                                                                 complement (<36507. ,>36887)
/gene="JPH3"
/note="synonym: JP3"
                                                                                                                                                                                                                                                                    complement(<36507. .>36887)
/gene="JPH3"
/product="junctophilin 3"
                                                                                                                                                                                                                                                                                                                       complement (<36507. .36887)
                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
product="junctophilin 3"
                                                                                                                                                                  complement (35581. ,35746)
                                                organism="Homo sapiens"
                                                              Ltype="genomic DNA"
xref="taxon:9606"
                Location/Qualifiers
                                                                                                                                                                                      'rpt_type=tandem
                                                              /mol_type="genom:
/db_xref="taxon:
/chromosome="16"
                                                                                                                                                                                                    unit="ctg'
Institutions,
                                                                                                                                                                  repeat_region
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SMIKSKGSKGKKKKKKRSGSMISSCYYYSASSCMWMMSSKSCMCCCMMMKRRCACCYSSM 17781
17661
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/db_xref="G1:6731722"
/db_xref="REWTREMBL:CAB69190"
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AAVDAHGAARALEMHGINFAPRGTKSELTVAEWIRHHIDHLTGVEQYTIDKYEGYLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RYLSTNPASGRRLPRGNAEDDDEIRMLTHAEFDRLRDAVTPHWKLMVQFMVSTGLRWG
SVALOPRHYDLETSTIRWADAWKS SAGYULDEPBYKTKRSRRYDVPARLLERLDLSN
EVVEVNTDGGEVRY POETLRRVWNPAVERAGIVPRPTPHDLRHTYASWQLTGGTPVTIV
SRQLGHESIQITVDTYTDVDRTSSRVAAEFMDGLLGDF"
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                                                                                                                                                                                                                                                                                                                                                              SCISMYRCCWGGMKSYSICGTICKKCIGYKKSRIWYWWYSWISKMYMWRAACMMYC 17838
                                                                                                                                                                                                                                                                                                                                        GATCCTGATTTCTGCCGGGCGTCCGCTGTCGGCGATCTCCCGGCCGCCTCGGTCACTC 1019
                                                                                                                                             SKYYYYCTGRRAMMTYMCCCWRRRSYMYYRSMSAMGMRKSSWSGMRAMGSASSRRCKSA
                                                                                                                                                                                                                 SESSWCSRRWKGMRGSCWSSKOWGGBRSRSASSKCKGSRGMRRRSKRSSKYRKRGRKKR
                                                                                                                      CGCGCCGAAAGGCGGGATGGTAAGGACGCGCAATTTCCGGCGGATCTGGGTCAAGGCGTG
                                                                                                                                                                                                                                                                CGAGGAAGCCGGGCTTCCG---GCTTACGCATTCACGATCTGCGGCACACTCACGCGC
                                                  GCTCGTCTTCCAGTCGCCGAAGACCGCGAAGGCCGGCGCCACGGTCAGTTTCACCACGAA
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Da.C.G., Freitas, V.A. and Trans-Complementation, U.A.
Patent: Wo 9907861-A 1 18-FEB-1999;
DA COSTA GARCIA MIGUEL ANNELO (PT); FREITAS VIEIRA ALCINO
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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/db_xref="taxon:65388"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 61.6; DB 6;
Pred. No. 12;
0; Mismatches 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2404 bp
Sequence 1 from Patent WO9907861.
A81401
A81401.1 GI:6731721
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/transl_table=11
/product="INTEGRASE"
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Mycobacterium phage
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Best Local Similarity 48.5°
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AUTHORS
JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                              PAT 22-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chang, H.S., Chen, W., Cooper, B., Glazebrock, J., Goff, S.A., Hou, Y.M., Karagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G. Plant genes involved in defense against pathogens
Patent: WO 03000898-A 5263 03-JAN-2003;
Syngenta Participations AG (CH)
1448 GGCCGCCGAAGACGAAACGGTCCCGCCGCACGGTGGATGTGCCGGCCAGGTTGTTGGAGC 1507
                                                                                               910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tracheophyta;
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                               TGCTTACGCCACTCATCGCCGGAAAGAAAAGTGACGAGGTCGTGTTCACCGCGCCGAAAG
                                                                GACTTGTCGAACGAGTTTGTTTTCGTCAATACCGATG
                                                                                               GCGGGATGGTAAGGACGCGCAATTTCCGGCGGATCTGGGTCAAGGCGTGCG-----AGG
                                                                                                                              1550 GTGGACCGGTCAGGTATCCGGGGTTTCTGCGTAGGGTGTGGAATCCGGCTGTGGAAGG
                                                                                                                                                             911 AAGCCGGGCTTCCGGGCTTACGCATTCACGATCTGCGGCACACTCACGCGGCGATCCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        593 SMKGSTRRSKMGRWSGMSRMYMRWWKKMRKRKYMRYMKWKCTWRRCMCYRWGYTMYTTSR
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Trach
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideee, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.1%; Score 60.4; DB 6;
llarity 10.7%; Pred. No. 19;
Conservative 277; Mismatches 263;
                                                                                                                                                                                                                                                                                                                                                                                               AX655393 2000 bp DNA
Sequence 5263 from Patent WO03000898.
AX655393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa"
/mol_type="unassigned DNA"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                              1031 TCACGGATCTGCTGTACGGGCACCTG 1056
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Best Local Similarity
Matches 65; Conserv
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Caranto, D. Marie, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Alsbrooks, S., Amin, A., Anguiano, D., Bandaranaike, D., Barber, M., Bacas, B. Baden, H., Benakaranike, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Blair, J., Blair, J., Blair, J., Barber, M., Barnstead, M., Benahmed, F., Cardenon, E., Cardenon, S., Changard, C., Cockrell, R., Cox, C., Coyle, M., Chen, Z., Chu, J., Claveland, C., Cockrell, R., Cox, C., Coyle, M., Chen, Z., Chu, J., Davila, M. L., Davis, C., Deramo, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Drapper, H., Dugar-Rocha, S., Deramo, C., Burch, P., Burch, P., Burch, P., Bares, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Farls, T., Fan, G., Fernandez, S., Filley, M., Elagy, N., Forbes, L., Foster, M., Garza, M., Gebregeorgis, S., Filley, M., Fladgen, N., Guerra, W., Gebregeorgis, S., Filley, M., Handley, M., Henderson, N., Hernandez, M., Havlak, P., Hawel, A., Handler, M., Hogues, M., Hollins, B., Howells, S., Hulaku, S.L., Hodgson, R., Hogues, M., Jackson, L., Jacob, L., Jang, H., Loohnson, B., Johnson, R., Marja, M., Johnson, B., Johnson, R., Marja, M., Johnson, B., Johnson, R., Marja, H., Lewan, J., Lewis, L., Lougez, J., Lorensuhwa, L., Loulesged, H., Lorado, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Mandum, B., Mapum, P., Martin, K., Martin, R., Mandum, P., Martin, R., Martin, R., Martin, R., Palak, S., Palak, R., Perez, M., Peres, K., Regier, M., Peres, K., Regier, M., Peres, K., Regier, M., Peres, K., Regier, M., Peres, S., Peres, K., Regier, M., Peres, M., Peres, K., Regier, M., Peres, S., Relly, M., Ren, Y., Reute
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Rattus norvegicus clone CH230-229C14, WORKING DRAFT SEQUENCE.
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561 CACGGCGCTTCCGCCGCACTGGCGACCGCTCGTCATGCTGCTGGTGGCGACCGGTCTGAG 620
                                                                                                                                                                                                  234
                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTGACCGTCGTCGAGCAGCTCCAGGAGCTGGCCAGCACGGGAGAGCTCGTCTTCCAGTC 740
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 SMMRTAGKWKWRSWSRWCRSYSWYKMYKKOWKKSYYMSYGWARSSGTWSRSAAKRTYKGY
                                                                                                                                                                                                                                                                                    HTGS_FULLTOP
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Rattus norvegicus
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AC130981.3 GI:30578466
HTG; HTGS PHASE2; HTGS I
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Submitted (16-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, USA

Sat Genome Sequencing Consortium.

Direct Submission

Direct Submission
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbern, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Strong, Y., Strong, R., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Walder, M., Walker, B., Wang, J., Wang, Q., Warren, U., Warren, R., Warlen, Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, U., Yoon, V., Weinstock, G. and Gibbs, R.A., Smith, D. R., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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NOTE: This is a "working draft' sequence It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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Consensus quality: 216581 bases at least Q40
Consensus quality: 218902 bases at least Q30
Consensus quality: 2203535 bases at least Q20
Estimated insert size: 225199; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
------- project Information
Center project name: GYQ
Center clone name: CH230-229C14
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Center code: BCM
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/db xref="taxon:10116"
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1 (bases 1 to 258319)

Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Alsbrooks, S., Amin, A., Anguiano, D., Allen, E., Asbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Benahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barastead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barastead, M., Benahmed, F., Carter, K., Cavazos, I., Censar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Coyle, M., Cree, A., D'Souza, L., Davis, C. Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Dunn, A., Dutahla, T., Fan, G., Fanner, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Garza, M., Gebrageorgis, E., Gerk, G., Gardy, M., Guerra, W., Guerra, W., Gebrageorgis, E., Garla, R., Hander, M., Hamil, C., Hamilton, K., Harnandez, S., Haland, M., Hamil, C., Hamilton, C., Hamilton, K., Harnandez, R., Hanes, A., Handers, M., Holbis, S., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Hernandez, R., Hines, S., Hlauw, S.L., Hodgson, A., Hodges, M., Garze, C., Kowis, C., Karft, C.L., Lebow, H., Levan, J., Lewis, L., Liu, J., Liu, M., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, M., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, M., Liu, Y., London, R., Malloy, K., Mangum, A., Mangum, P., Martin, K., Martin, S., Mundeshen, E., Manderris, K., Morris, S., Mundeshen, E., Manderris, C., Okwion, G., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, L., Perez, L., Perez, R., Perez, L., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222692 GGTGGAĞĞAĞĞAĞATĞGAĞĞAĞATĞGAĞĞAĞAĞATĞĞAĞĞAĞĞAĞAĞTĞGAĞĞAĞĞA 222751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1089 GATCGAGGAGGCGAIGGCCGGCGTCCGGGCTGAGGACCTGGAGGCGGAACTCGACGAGGA 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC127770 258319 bp DNA linear HTG 10-OCT-2002
Rattus norvegicus clone CH230-94P3, WORKING DRAFT SEQUENCE.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 7.6;
0; Mismatches 52; Indels 0;
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Rattus norvegicus (Norway rat)
Rattus norvegicus
                              1. .1186
/note="wgs_contig"
complement(229055. .229809)
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                                                                                                                                                                                                                                                    end_sequence:BZ108940"
/clone="CH230-229C14"
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                                                                                                                                             'note="clone boundary
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                                                                                                                                                                    clone end: Sp6
site: EcoRI
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Matches 91; Conservative
                                          misc_feature
                                                                                                           misc_feature
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AC127770
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DEFINITION
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La Submitted (10-007-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, USA

Do Oct 10, 2002 this sequence version replaced gi:21908142.

The sequence in this assembly is a combination of BAC based reads and whole genome shorpun sequencing reads assembled using Atlas (http://www.hgsc.bom.tmc.edu/projects/rat/). Each config described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ms to the estimated size. The sequence contigs within a contigy scaffold that consist entirely of whole genome shorgun sequence reads. Both end sequences and whole genome shorgun sequence reads. Both end sequences and whole genome shorgun sequence reads. Both end sequences and whole genome shorgun sequence reads. Both end sequences and whole genome shorgun sequence reads. Both end sequences and whole genome shorgun sequence reads. Both end sequences and whole genome shorgun sequence reads. Both end sequences and whole genome shorgun sequence only contigs will be indicated in the feature
Plopper, F., Poindexter, A., Popovic, D., Frimus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Sheats, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Sheats, W., Strong, R., Sutton, A., Satek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, T., Usmani, K., Valas, R., Varas, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, G., Williams, G., Wilson, R., Warch, R., Wooden, H., Worley, K., Williams, G., Wilson, R., Warch, S., Van, J., Yoon, L., Yoo, Yu., Yu., Zhang, J., Zhou, J., Zhou, S., Dunn, D., Von Niederhausern, A., Weiss, R., Smith, D., R., Smith, H.O., Direct Submission

L. Unpublished

E. (Dases I to 258319)
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NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (Jasses 1 to 258319)
Rat Genome Sequencing Consortium.
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 258319: contig of 258319 bp in length.
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Contact: hgsc-help@bcm.tmc.edu
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121399 GATGGAGGAGGCGATGGAGGCGATGGAGGAGAGATGGAGGAGGAGGAGGAGGAGGA 121458
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Penicillium marneffei STS, clone pm7g11.b, sequence tagged site.
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Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Penicillium.
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Cal,J.J., Cheung,E.Y., Medigue,C. and Danchin,A.
Exploring the Penicillium marneffei genome
Arch. Microbiol. 179 (5), 339-353 (2003)
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63.6%; Pred. No. 7.4;
tive 0; Mismatches 52;
                                                 1. 1335
/note="wage end extension
clone end:177" at 2017. 6806
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256123. .258319
/note="wgs_end_extension
clone_end:T7"
                                                                                                                                                                                                                                                                                                                                                                                                                 /note="wgs_end_extension
                                                                                                                                                                                                                                                                                      /organism="Rattus norve
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/db_xref="taxon:10116"
/clone="CH230-94P3"
                                                                                                                     3017. .68966
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clone end:T7
site:EcoRI
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3050, 3950
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12645. .13876
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clone_end:T7
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/note="clone boundary
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Danchin,A. and Pascal,G.
Direct Submission
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AL685196.1 GI:19337723
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artificial sequences; vectors.

1 (bases 1 to 3689)
Kropinski, A.M., Hungy,V.Y.-F., Kim,D. and Yung,E.
Characterization of the int-att region of bacteriophage D3, and the attD3 site on the Pseudomonas aeruginosa genome
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LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
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               Kropinski, A.M., Huang, V.Y.-F., Kim, D. and Yung, E. Direct Submission
Submitted (26-APR-2000) Microbiology and Immunology, Queen's University, Room 741, Bottell Hall, Kingston, Ontario K7L 3N6, Canada
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                                                                                                                                                                                               /organism="Integration vector
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3897..1249
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Pred. No. 23;
0; Mismatches
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/mol_type="other DNA"
/db_xref="taxon:135522"
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protein_id="AAG01407.1"
db_xref="GI:9885347"
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/gene="bla"
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/gene="int"
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Botterell Hall, Kingston,
741/743, Botterell Hall, Kingstc
11 (bases 1 to 7657)
Kropinski,A.M. and Gilakjan,M.A.
Direct Submission
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/gene="orf3"
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2264. .3568
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Kropinski, A.M., Huang, V.Y.-F., Kim, D. and Yung, E.
Characterization of the int-att region of Bacteriophage D3, and the
attD3 Site on the Pseudomonas aeruginosa genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gilakjan, Z.A. and Kropinski, A.M.
Cloning and analysis of the capsid morphogenesis genes of
Pseudomonas aeruginosa bacteriophage D3: another example of protein
                                                        PHG 23-OCT-2000
                                                                                                                                                                                             Pseudomonas phage D3
Pseudomonas phage D3
Viruses, dsDNA viruses, no RNA stage, Caudovirales, Siphoviridae,
Lambda-like viruses.
Rambda-like viruses.
Rambda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Topses 53297 to 54321)

Kropinski,A.M. and Sibbald,M.J.

Transfer RNA genes and their significance to codon usage in the Pseudomonas aeruginosa lamboid bacteriophage D3

Can. J. Microbiol. 45 (9), 791-796 (1999)
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Direct Submission
Submitted (04-440-1993) Microbiology, Queen's University, F 741/743, Botterell Hall, Kingston, Ontario K7L 3N6, Canada B (bases 46478 to 46764)
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Kropinski, A.M. and Sibbald, M.J.
Direct Submission
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                             56425 bp DNA linear PHG.
Bacteriophage D3, complete genome.
AF165214 L22692 U32623 U47623 AF077308 AF147978 AF165213
AF165214.1 GI:8895104
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Kropinski, A.M. and Sharp, R.W.
Direct Submission
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JOURNAL
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  RESULT 15
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                                                                                                                                                                                                        Queen's University, Room 743,
3N6, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            743,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On or before Jul 2, 2000 this sequence version replaced gi:403435, gi:984852, gi:1685011, gi:4927380, gi:5059247, gi:6166381. Location/Qualifiers
                                                                                                                                                                                                   Submitted (04-WAY-1999) Microbiology, Queen's University, Room 74 Botterell Hall, Kingston, Ontario K71 3N6, Canada
12 (Bases 26775 to 28246)
Kropinski,A.M., Huang,V.Y.-F., Kim,D. and Yung,E.
Direct Submission
Submitted (03-UIL-1999) Microbiology, Queen's University, Room 74 Botterell Hall, Kingston, Ontario K71 3N6, Canada
13 (Bases 1 to 56425)
Kropinski,A.M.
Butterell Hall, Mingston, Ontario K71 3N6, Canada
Submitted (05-UIL-1999) Microbiology & Immunology, Queen's Submission, Ontario K71 3N6, University, Room 741, Botterell Hall, Kingston, Ontario K71 3N6, University, Room 741, Botterell Hall, Kingston, Ontario K71 3N6,
Ontario K7L 3N6, Canada
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419. :2110
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EHKGKVTVNIIGLAASAASFIAMAGDEIRIGRAAFLMIHNAMLIAMGNRNDLREIADW
LEPFDWTLADIYAQRTEIDIDDIVKQMDAETWIGGREAVDKGWADAFLESDEISSAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to Escherichia coli bacteriophage HK97 major head protein: SwissProt Accession Number P49861; proteolytically processed and cross-linked in mature phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MBDFEKQIGELNASLKQVGDQIKSQAEQVNTQIANFGEMNKETR
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QLAEFPASGIVLNPIDWALIELNKDAENRYIIGSPQNGTTPTLWRLFVVSTQAITQDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRSEAILAKRRMDAALARSGMPRSQRNELINDFKTSMLGAAGGGGDTPTDMPGAVAPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3572. 4462
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2264. .3568
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portal protein: SwissProt Accession Number P49859"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="major head protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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                                                                                                                       start=1
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Matches 90; Conserv
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Search completed: August 6, 2004, 11:53:05 Job time : 5421.76 secs

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Sequence 112, Appl
Sequence 11386, A
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Sequence 1, Appli
Sequence 12882, A
Sequence 12882, A
Sequence 12882, A
Sequence 12720, A
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4617.079 Million cell updates/sec
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Sequence 34,
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                             OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Perfect score:
Sequence:
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845 CCGCGCCGAAAGGCCGGGATGGTAAGGACGCGCAATTTCCGGCGGAATCTGGGTCAAGGCGT 904
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Sequence 34, Application US/09183861
Patent No. 6386165
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Stalton, Davin C.
APPLICANT: Stalton, Laise, NW.
TITLE OF INVENTION: LEISHVANIA ANTIGENS FOR USEIN THE THERAPY AND NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 51.4; DB 4; Length 516; Pred. No. 0.036;
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APPLICATION NUMBER: US/09/183,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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RAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1085 CGGCGATCGAGGAGGCGATGGCCGGCG
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,765
FILING DATE: 12-FEB-1998
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INFORMATION FOR SEQ ID NO: 34
SEQUENCE CHARACTERLETICS:
LENGTH: 516 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity
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US-09-183-861-34
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APPLICANT: Hosted Jr., Thomas J.
TILLE OF INVENTION: Isolated Nucleic Acids from Micromonospora rosaria
TILLE OF INVENTION: plasmid pMR2 and Vectors Made Therefrom
TILLE OF INVENTION: plasmid pMR2 and Vectors Made Therefrom
TILLE OF INVENTION: plasmid pMR2 and Vectors Made Therefrom
TILLE PREPERBORE.
TILLE PREPERBORE.
TOOR OF SECTION NUMBER: US/09/821,167
CURRENT APPLICATION NUMBER: US 60/194,461
PRIOR FILING DATE: 2000-04-04
NUMBER OF SECID NOS: 15
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Pred. No. 0.0043;
0; Mismatches 299; Indels
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Patent No. 6569668
GENERAL INFORMATION:
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ORGANISM: Micromonospora rosaria
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Best Local Similarity 46.2%;
Matches 262; Conservative
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; LOCATION: (10010)..(10012)
US-09-821-167-1
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LOCATION: (6055)..(6059)
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(6391)..(6394)
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SEQ ID NO 1
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                                                                      302 AGCTGGACGGGCAGGTCACCCAGCAGTGGGTCAACGACCTGGAGGCCGGCGTCGGCCGGT
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   Gaps
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APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
NUMBER OF SEQUENCES: 87
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   Mismatches 246; Indels
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ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,765
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12-FEB-1998
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Patent No. 6375955
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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   Conservative
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APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERANY AND DIAGNOSIS OF LEISHMANIASIS
FILE REPERENCE: 210121.420C5
CURRENT APPLICATION NUMBER: US/09/551,974A
CURRENT APPLICATION SOO0-04-14
NUMBER OF SEQ ID NOS: 101
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 0.036;
0; Mismatches 246;
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47.1%; Pred. No. 0.036;
tive 0; Mismatches 246;
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                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                 Leishmania major
                                                                                                                                                                                                              Query Match 4.4%;
Best Local Similarity 47.1%;
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity
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                                                                                                                                 ORGANISM:
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APPLICANT: Reed, Seven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Wiebb, John R.
APPLICANT: Mish, Javin C.
APPLICANT: Blatia, Ajay
APPLICANT: Blatia, Ajay
APPLICANT: Coler, Rhea
APPLICANT: Coler, Peter
ITILE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
ITILE OF INVENTION: THERMAY AND DIAGNOSIS OF LEISHMANIASIS
FILE REPERENCE: 210121.42067
CURRENT APPLICATION NUMBER: US/09/639,206A
CURRENT FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FRASEC for Windows Version 4.0
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Pred. No. 0.036;
0; Mismatches 246;
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ORGANISM: Leishmania major
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APPLICANT: Gampos-Neto, Antonio
APPLICANT: Gabb, John C.
APPLICANT: Billion, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Blatia, Ajay
APPLICANT: Colar, Rhatia, Ajay
APPLICANT: Peter Probst
TITLE OF INVENTION: ILESCHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: ILESCHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REPERENCE: 210121.420C6
CURRENT APPLICATION NUMBER: US/09/565,501A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 47.1%; Pred. No. 0.036;
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APPLICANT: Webb, John R.
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APPLICANT: Skeiky, Yasir A.W.
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APPLICANT: Coler, Rhea
APPLICANT: Probst, Peter
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APPLICANT: TREADAY AND DIAGNOSIS OF LEISHMANIASIS
TITLE OF INVENTION: LEISHMANIA ANTIGENS OF LEISHMANIASIS
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
CURRENT FILIKG DAFE: 2001-06-04
CURRENT FILIKG DAFE: 2001-06-04
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
TUBEL OF INVENTION: LEISHMANIASIS
FILIKG SAFIRMANIASIS
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APPLICANT: Campos-Neto, A
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GENERAL INFORMATION:
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APPLICANT: Webb, John R.

APPLICANT: Blatia, Ajay
APPLICANT: Bhatia, Ajay
APPLICANT: Bratia, Ajay
APPLICANT: Coler, Rhea
APPLICANT: Branch, Mark
APPLICANT: Branch, Mark
APPLICANT: Branch, Mark
APPLICANT: Branch, Mark
APPLICANT: Branch, Wark
APPLICANT: ABRICANTON LEISHWANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: LEISHWANIASIS
FILE REPERENCE: 210121.420C8
CURRENT APPLICANTON NUMBER: US/09/874,923
CURRENT PILICA DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 114
LENGTH: 582
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US-09-874-923-114
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Patent No. 6538517
PAPPLICANT: Reed, Steven G.
S-09-874-923-114
Sequence 114, Application US/09874923
Patent No. 6638517
                                                                                                                                                                                                                                                              APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
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Best Local Similarity 47.1%;
Matches 222; Conservative
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4.4%; Score 51.4; DB 4; Length 7065;
Best Local Similarity 47.1%; Pred. No. 0.048;
Matches 222; Conservative 0; Mismatches 246; Indels 3
                                            APPLICANT: Brain, Davin C.
APPLICANT: Brain, Ajay
APPLICANT: Brain, Ajay
APPLICANT: Coler, Ajay
APPLICANT: Coler, Rhea
APPLICANT: Coler, Rhea
TITLE OF INVENTION: LEISHWANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: LEISHWANIA ANTIGENS OF LEISHWANIASIS
FILE REPERENCE: 210121.42008
CURRENT APPLICATION NUMBER: US/09/874,923
CURRENT APPLICATION NUMBER: US/09/874,923
CURRENT FILE OBS. 122
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FRESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA CORGANISM: Ceishmania major and chagasi US-09-874-923-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09679279; Patent No. 6524841; GENERAL INFORMATION:
Campos-Neto, Antonio
Webb, John R.
                                                                                                                                                                                                                                                                                                                                                                                                                     7065
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US-09-679-279-1
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SEQ ID NO: 5= translated amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  megDIV, TDP-4-keto-6-deoxyglucose 3,5-epimerase (eryBVII, dnmU
TDP-4-keto-6-deoxyhexose 3,5-epimerase;
SEQ ID NO: 8= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..(9220)
1: megBII-1(megDVII), TDP-4-keto-L-6-deoxy-hexose 2,3-reductase;
1: SEQ ID NO: 10= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          megBV, mycarosyl transferase, mycarose glycosyltransferase, SEQ ID NO: 11= translated amino acid sequence
                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (1)...(144)
OTHER INFORMATION: megBVI(megT), TDP-4-keto-6-deoxyglucose-2,3-dehydratase,
OTHER INFORMATION: SEQ ID NO: 2= translated amino acid sequence
LOCATION: (928)...(2061)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     megDV, TDP-hexose 4-ketoreductase (eryBIV, dnmV homolog), TDP-4-keto-6-deoxyhexose 4-ketoreductase; SEQ ID NO NO: 9= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                megDII, deoxysugar transaminase (eryCI, DnrJ homolog)
TDP-3-keto-6-deoxyhexose 3-aminotransaminase;
SEQ ID NO: 6= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: (12181)...(22821)
OTHER INFORMATION: megAI; SEQ ID NO: 13= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           megDI, rhodosaminyl transferase (eryCIII homolog),
TDP-megosamine glycosyltransferase,
SEQ ID NO: 4= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: megDVI, TDP-4-keto-6-deoxyglucose 3,4-isomerase, OTHER INFORMATION: TDP-4-keto-6-deoxyhexose 3,4-isomerase; OTHER INFORMATION: SEQ ID NO: 3= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: megEIV, TDP-hexose 4-ketoreductase, OTHER INFORMATION: TDP-4-keto-6-deoxyhexose 4-ketoreductase; OTHER INFORMATION: SEQ ID NO: 12= translated amino acid sequence
          NUMBER OF SEQ ID NOS: 34 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
                                                                                              LENGTH: 47981
TYPE: DNA
ORGANISM: Micromonospora megalomicea
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OTHER INFORMATION: megAI, ACP-L
NAME/KEY: misc_feature
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OTHER INFORMATION: megAI, AT-L
2000-03-17
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OTHER INFORMATION: megA1, KS1
NAME/KFY: misc_feature
LOCATION: (15427)...(1476)
OTHER INFORMATION: megA1, AT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (9226) ... (10479)
OTHER INFORMATION: megBV, m
OTHER INFORMATION: SEQ ID N
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OTHER INFORMATION: megG(mcOTHER INFORMATION: SEQ ID
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SEQ ID NO: 15= translated amino acid sequence
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OTHER INFORMATION: megAII, KR3 (inactive)
NAME/KEY: misc_feature
LOCATION: (26998)...(27258)
OTHER INFORMATION: megAII, ACP3
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LOCATION: (17155)...(17694)
OTHER INFORMATION: megAl, KR1
NAME/KEY: misc feature,
LOCATION: (17947)...(18207)
OTHER INFORMATION: megAL, ACP1
NAME/KEY: misc feature
LOCATION: (18268)...(19548)
OTHER INFORMATION: megAL, KS2
NAME/KEY: misc feature
LOCATION: (19876)...(20910)
OTHER INFORMATION: megAL, AT2
NAME/KEY: misc feature
LOCATION: (19876)...(20910)
OTHER INFORMATION: megAL, AT2
NAME/KEY: misc feature
LOCATION: (21517)...(22053)
OTHER INFORMATION: megAL, KR2
NAME/KEY: misc feature
LOCATION: (21517)...(22053)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (22957) ... (24237)
OTHER INFORMATION: megAII, KS3
NAME/KEY: misc feature
LOCATION: (24544) ... (25581)
OTHER INFORMATION: megAII, AT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (27393) ...(28590)
OTHER INFORMATION: megAII, KS4
NAME/KEY: misc feature
LOCATION: (28897) ...(29931)
OTHER INFORMATION: megAII, AT4
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LOCATION: (39795)...(40811)
OTHER INFORMATION: megAIII, AT6
NAME/KEY: misc_feature
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OTHER INFORMATION: megAII, ACP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (22867)...(33555)

OTHER INFORMATION: megAII; SEQ
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CTHER INFORMATION: megAll, KR4

NAME/KEY: misc feature

LOCATION: (33052)...(33312)
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LOCATION: (29953)...(30477)
OTHER INFORMATION: megAII, DH4
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NAME/KRI: m.isc. featuri, CLOCATION: (31396)...(32244)
OTHER INFORMATION: megali, ER4
                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (22318)...(22575)
OTHER INFORMATION: megAI, ACP2
NAME/KEY: CDS
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LOCATION: (3768)...(3764)
OTHER INFORMATION: magalli, KI
NAME/KEY: misc feature
LOCATION: (37860)...(3812)
OTHER INFORMATION: magalli, AI
NAME/KEY: misc feature
LOCATION: (38187)...(39470)
OTHER INFORMATION: magalli, KI
NAME/KEY: misc feature
LOCATION: (38187)...(39470)
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OTHER INFORMATION: megAIII;
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OTHER INFORMATION: megAIII,
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LOCATION: (35385)...(36419)
OTHER INFORMATION: megAIII,
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LOCATION: (33780)...(3
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; LOCATION: (47411)...(47980)
; OTHER INFORMATION: megF, C-6 hydroxylase; SEQ ID NO: 20= translated amino acid seque
US-09-679-279-1
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SEQ ID NO: 17= translated amino acid sequence
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OTHER INFORMATION: megH, TEII; SEQ ID NO: 19= translated amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                           megCII, TDP-4-keto-6-deoxyglucose 3,4-isomerase; SEQ ID NO: 16= translated amino acid sequence
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RMATION: megBII-2(megBII), TDP-4-keto-6-deoxy-L-glucose
RMATION: TDP-4-keto-6-deoxyglucose 2,3 dehydrarase;
RMATION: SEQ ID NO: 18= translated amino acid sequence
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Pred. No. 0.096;
0; Mismatches 276; Indels 15;
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Best Local Similarity 46.3%;
Matches 251; Conservative
OCHER INFORMATION: megalii, NAME/KEY: misc feature
                                                                                                                                         LOCATION: (42168)...(42425)
OTHER INFORMATION: megAIII,
                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (42585)...(43271)
OTHER INFORMATION: megAIII,
                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (43268)...(44344)
OTHER INFORMATION: megCII,
OTHER INFORMATION: SEQ ID NO
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687 CGTCGTCGAGCAGCTCCAGGAGCTGGCCAGCACGGAGAGACTCGTCTTCCAGTCGCCGAA 746
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Patent No. 6531795
GENERAL INFORMATION:
PAPLICAMTH MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11487
                                                                                      Sequence 11386, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILIATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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Best Local Similarity 46.2%;
Matches 166; Conservative
                                              09-252-991A-11386/c
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US-09-252-991A-11487
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US-09-252-991A-11487
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RESULT 14
US-09-252-91A-11405/C

1 Sequence 11405, Application US/09252991A

2 Retent No. 6521795

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION:

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Score 50.2; DB 4;
Pred. No. 0.078;
0; Mismatches 193;
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US-09-252-991A-11405
4.3%;
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Conservative
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Best Local Similarity
Matches 166; Conserva
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us-09-855-340a-1.rni

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RESULT 15
US-09-252-91A-2186
US-09-252-91A-2186
Sequence 2186, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT MACE J. RUDenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ASSUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 915
1218 GATCGCCAGGACCATGCCGAACATGGTCAGCACGTTGATCGAGAAGCCCAGGCAT 1159
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4.1%; Score 48.8; DB 4; Length 915;
Best Local Similarity 51.1%; Pred. No. 0.13;
Matches 140; Conservative 0; Mismatches 132; Indels
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Search completed: August 6, 2004, 13:42:24 Job time : 147.71 secs

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GenCore version 5.1.6
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<pre>Run on: August 6, 2004, 08:50:04 ; Search time 1956.12 Se</pre>	Seconds 1 updates/sec
Title: VS-09-855-340A-2 Perfect score: 426 Sequence: 1 atgcgcaacacccggggctacctgttccgccggagctga	ıgctga 426
Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	
Searched: 3470272 segs, 21671516995 residues	
Total number of hits satisfying chosen parameters: 6940544	-11
Minimum DB seq length: 0 Maximum DB seq length: 2000000000	
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database : GenEmbl:*  1: gb_ba:*  2: gb_on:*  4: gb_on:*  5: gb_ov:*  6: gb_ph:*  10: gb_pr:*  11: gb_pr:*  12: gb_sr:*  12: gb_sr:*  13: gb_r:*  14: gb_sr:*  15: em_ba:*  16: em_bu:*  17: em_ba:*  18: em_in:*  19: em_ov:*  22: em_ov:*  23: em_ov:*  24: em_ph:*  25: em_ov:*  25: em_ov:*  26: em_for:*  27: em_for:*  28: em_ro:*  28: em_ro:*  29: em_ro:*  29: em_ro:*  29: em_ro:*  29: em_ro:*  29: em_ro:*  29: em_ro:*  20: em_for:*  20: em_for:*  20: em_for:*  20: em_ro:*  20: em_ro:	

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Micromonospora halophitica and Micromonospora carbonacea chromosome Patent: WO 0187936-A 2 22-NOV-2001; SCHERING CORPORATION (US)
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                                                                                                                                                                                                                                                 GAGCGCCCGGACTGACCAAGAGCGAGTTGGCCAGGCGCATCCAGAAGGACCGGGCCACC
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                                                                                                                                                                                           Gaps
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Hosted, T.J., T.L., Alexander, D.C. and Hewitt, D.D.
Burset Submission

Bubmitted (12-SEP-2002) New Lead Discovery, Schering-Plough
Sesearch, 2015 Galloping Hill Road, Kenilworth, NJ 07033, USA
Location/Qualifiers
1. 2028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in Micromonospora spp
Microbiology (Reading, Engl.) 149 (Pt 9), 2443-2453 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alexander, D.C., Devlin, D.J., Hewitt, D.D., Horan, A.C. and
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                                                                                                                                        Length 426;
                                                                                                                                                                 Indels
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    426
        /organism="Micromonospora carbonacea"
        /mol type="unassigned DNA"
        /db_xref="taxon:47853"

                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e-42;
Matches 426; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Bacteriophage pMLP1"
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Bacteriophage pMLP1 att/int region.
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Bacteriophage pMLP1
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KEYWORDS
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197 . 622

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PCSSTWLRREPKEMRKELSDPBIGRLITALPPHWRELWMLLVATGLEWGBAIGLRAGR
VDLLAARPRLITVVEQLQELASTGELVFQSPKTAKGRRTVSFTTKVALLITPLIAGKKS
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RRLGHSSIAVTDLLYGHLREEVDEGILAAIEEAMAGVRAEDLEAELDEELTDVLADAA
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100.0%; Pred. No. 3.5e-42;
tive 0; Mismatches 0;
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/note="attP element"
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/note="att/int region"
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/transl_table=:
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The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N. Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I. Kojima, K., Namiki, T., Chneda, E., Yahaqi, W., Suzuki, K., Li, C., Ohtsuki, K., Ishishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Kurosaki, T., Kodama, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Kurosaki, T., Kodama, T., Masuno, K., Yokomizo, S., Niikura, J., Narikawa, R., Sugano, S., Fujimura, T., Suzuki, Y., Yokomizo, S., Niikura, J., Kawami, J., Kawamata, M., Yoshimura, A., Miuta, J., Kawai, J., Carninoi, P., Adachi, J., Alazawa, K., RIKEN:, Kawai, J., Koan, M., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Shibata, K., Shinagawa, A., Shizaki, T., Yohino, M. and Hayashizaki, Y., Shibata, K., Shinagawa, A., Shizaki, T., Yohino, M., and Hayashizaki, Y., Shibata, K., Shinagawa, A., Shizaki, T., Yohino, M., Shizaki, T., Yohino, M., Shizaki, T., Yohino, M., Shizaki, T., Yohino, M., Shizaki, T., Shibata, K., Shinagawa, A., Shizaki, T., Yohino, M., Shizaki, T., Shibata, K., Shinagawa, A., Shizaki, T., Yohino, M., Shizaki, T., Shinagawa, A., Shizaki, T., Shinagawa, A., Shizaki, T., Yohino, M., Shizaki, T., Shinagawa, A., Shiza
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Oryza sativa (japonica cultivar-group) cDNA clone:J023102B22, full insert sequence.
AK121255
AK121255.1 GI:37990878
FILZCDNA, "CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Susaryota, "viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermarcophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryza.
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LAIL JUNZO, TAKAHARA MASAYASU, PI
LAIL 2) 55, CIZNI/19, CIZNI/21, CIZNI/19, CIZNI/19, CIZNI/19, CIZNI/21, CIZNI/19, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI/21, CIZNI-125); CC
topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC anti-sense: No;
CC *Source: developmental_stacr
CC *Source: developmental_stacr
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(bases 1 to 1575)

Houriyou,K., Mizoguchi,J., Takahara,M., Imamura,S., Beppu,T. and Horinouchi,S.

DNA CONTAINING GENETIC INFORMATION OF PHOSPHOLIPASE AND USE THERE Patent: JP 1991187382-A 1 15-AUG-1991;
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PI BEPPU TERUHIKO, HORINOUCHI SUEJI
PC C12N15/55,C12N1/19,C12N1/21,C12N9/20,(C12N1/19,C12R1:865),
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/organism="Streptomyces
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URL: http://cdaool.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length CDNA Project Tender. Kikuchi,S., Satch,K.,
Nagata,T., Kawagasahira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,B., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
Yamamoto,M. and Nakahama,Y.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,X.,
Kobayashi,M., Kodama,T., Rhibiki,J., Kawamada,M.,
Kobayashi,M., Kodama,T., Mizuno,K., Narikawa,R., Nikura,J., Oka,M.,
Ryu,R., Suganon,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M.,
Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Science Lebratory in Riken Genomic Science Lebratory in Riken Adachi,J., Alzawa,K.,
Aximura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Itoh,M., Kagawa,I., Kanagawa,S., Katch,H., Kawai,J.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Saloch,H., Sarai,D., Sato,K., Shibata,K.,
Shinaqawa,A., Shiraki,T., Sasaki,D., Sato,K., Shibata,K.,
Tagami-Takeda,Y., Tagawa,A., Takahashi,R.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.
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                                                                                                Direct Submission

Direct Submission

Submitted (31-79h-2003) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki
205-6602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fas.81-29-838-7007, This clone is one of the 32K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 GCCAGGCGCATCCAGAAGGACCGGGCCACCGTCGGCCGGTGGGAGGACGGCAAGAACCGG 150
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/mol type="mRNA"
/mol type="mRNA"
/db vare="taxon:39947"
/clone="J023102B22"
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3 (bases 1 to 1653)
Kikuchi, S.
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OSJN00062 124629 bp DNA linear PLN 30-NOV-2003
Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBb0108J11,
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Nature 420 (6913), 316-320 (2002)
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Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/), genscan (http://CGR-081.mit.edu/GENSCAN.html), GeneMarkHMM (http://genemark.biology.gatech.edu/GeneMark/), tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/), searches of the complete sequence against NCBI none redundant protein database (nr) (ftp://ncbi.nlm.nih.gov/blast/db) and the EST database at NCGR.
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Submitted (08-SEP-2001) Han Bin, National Center for Gene Research,
Chinese Academy of sciences, 500# Cao Bao Road, Shanghai 200233,
CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone requests:
                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, Liliopsida; Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Tu,Y.F., Jia,J., Yin,H.F., Zhang,Y., Cai,Z., Chen,J., Kang,H.,
Then,X.Y., Shao,Y., Sun,Y., Hu,Q.P., Zhang,X.L., Zhang,M.,
Wang,L.J., Ding,C.W., Sheng,H.H., Gu,J.L., Chen,S.T., Ni,L.,
Zhu,F.H., Han,B., Feng,Q., Huang,Y.C., Li,Y., Zhu,J.J., Zhao,Q.,
Hu,X., Liu,Y.L., Mu,J., Yu,Z., Chen,L., Fan,D.L., Weng,Q.J.,
Zhang,L., Lu,Y.Q., Yu,S.L., Liu,X.H., Lu,T.T., Zhang,Y.J., Lu,Y.,
Li,C., Li,T., Zhang,Y., Hu,H., Jia,P.X., Qian,Y.M., Ying,K.,
Zhu,B., Chen,Z.H., Hao,P., Zhang,L., Wu,M., Zhang,R.Q., Guan,J.P.
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/mol_type="genomic DNA"
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/gene="OSJNBb0108J11.1"
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| db_xref="taxon:39947"
| chromosome="4"
| clone="OSJNBb0108J11"
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                                                                                                               complete sequence.
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PKLQQSLIEQMLSHNNEIPGLISGGFMKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BKDPKEHKDPHHHBPKPEKPREHKDPAYTPPKPTPTPPTYTPKPTPKPTPKPTPRPTPTPRPTP
PAHTPTPPTYKPORFTPPTYROPKCTPAYTPPTPTPSYKPORKTPPTPPSYK
PKPTPTPTPTPPSYKPORFTPPTPSYKPORFTPPPSYKPOPKTPTPPPSYK
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KROORKPHPPTYKPORKRYPPTYKRAPPTYKROPKRYTPPTTYTPTYTPSY
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SEGEACVRVMGGVPC"
                                                                                                                                                                                                                                                                                                                      WSSSSPATSCDASVTSSPACIJVROVASPDĀDPSAALRQLAAYLSDDDVDEFEKNALVG
AGGAAEAVASVLRRKGEREVGVEGCEAAVRVLAAVVAMDGVEDANKRRVAAGLAADAA
ASAASLARVMRGASGLEARVDAARLVEFLLANAADEAREAVAESAELVAELVRLVGPA
                                                                                                                                                                                                                                                                                                                                                                                                                              DEKGSLDARAVGAGLSCLATISRSFRAARAEMYRAGTVRAAARALRATAADPAASARA
LRVLESSAVGCAEGRAALCEDAEQAVPAVVGRMMKAGRDGABAAAEAVIWAVCHKYRDRR
DADAAEASEGGLTRLLLLLQSGCSPAARQMALELLKIYKVNAKSCLAGYDSKTTHIMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 CCCGACGACGCGGACCTCGTTGCCCGGGTCGCCCAGGTGCTCGGCCTCGACCTCGACGAA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 GCCAGGCGCATCCAGAAGGACCGGGCCACCGTCGGCCGGTGGGAGGACGCCAAGAACCGG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCCTCGCCGCCGCAGGTCTGCGCCCCCGGCGTCACCCCGCCCAGCGACCCCAACCATGGAC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (68241. .72322)
/gene="OSJNBb0108J11.10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 124629;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTYTPTPPYHKPPPSYTPGPPPY"
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Pred. No. 12;
                                                                                                                                          protein_id="CAE02914.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="OSJNBb0108J11.7"
53985. .54338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="OSJNBb0108J11.7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53985. .54338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63156. .64238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .64238
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Best Local Similarity 49.6
Matches 166; Conservative
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29096. 3320cmilitarnoilliansoiselean

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33388. 33408)

33388. 33408)

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PIEHWHTPLVPCNMLTFKKGITLIGTSGISGSYVELRA
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IHLOEHIAKKILOFDDAMNDKKKLOOFLGLNYVARNHINNLAKIAGEDYAKLEKNGOR
YENSEDIKLYRLIKERVALEKPLELEBESYFIIETDASQHGMGAILKORPTKFSAKS
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LNSKKSSTRRWYLFEDIITGNGYKVIFEHIKGKDNNLPDMLSRLPELQLMKIMK"
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GGEEPGGAVIGAVVGEGGRQQLERHHRSRREQVR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oin(8822. .8969,9806. .10110,10231. .10416,11351. .11425,
.7124,7228. .7355,7446. .7838)
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/gene="OSJNBb0108J11.4"
35073. .3548?
                                                                                                                                                                                                                                                                                                                                                                                                           8822. .11803
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gene="OSJNBb0108J11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="OSJNBb0108J11.5"
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JP 2002537833-A/61.
Streptcmyces lavendulae
Streptcmyces lavendulae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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1 (bases 1 to 5350)
Sherman, D.H., Mao, Y., Varoglu, M., He, M. and Sheldon, P.C. Mitomycin biosynthetic gene cluster
Patent: JP 2002537833-A 61 12-NOV-2002;
REGENTS OF THE UNIVERSITY OF MINNESOTA
OS Streptomyces lavendulae
PN JP 2002537833-A/61
PD 12-NOV-2002
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Sherman, D.H., Mao, Y., Varoglu, M., He, M. and Sheldon, P.
Mitomycin biosynthetic gene cluster
Patent: US 6495348-A 66 17-DEC-2002;
Location/Qualifiers
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12-MAR-1999 US 09/266965
DAVID H SHERMAN, YINGQING MAO, MUSTAFA VAROGLU, MIN HE, PAUL C
                                                                                                                                                                                                                        17051 GTGGGCAGGATGATGAAGGCCGGCGCGCGCGCCCGCGGGGGCCGGGGGCCGTGCTATGG
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JP 2002537833-A/51.
Streptcmyces lavendulae
Streptcmyces lavendulae
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
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1 (bases 1 to 1056)
Sherman, D.H., Mao, Y., Varoglu, M., He, M. and Sheldon, P.C.
Mitomycin biosyntheiic gene cluster
Patent: JP 2002537833-A 51 12-NOV-2002;
REGENTS OF THE UNIVERSITY OF MINNESOTA
OS Streptomyces lavendulae
PN JP 2002537833-A/51
PD 12-NOV-2002
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Location/Qualifiers
1. .1056
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    1056
    70ganism="Streptomyces lavendulae"
/mol_type="genomic DNA"
/db_xref="taxon:1914"

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Mitomycin biosynthetic gene cluster.
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123. .1367
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/transl_table=11
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,C12Q1/68,G01N33/53,
PC G01N33/566//C12N9/00,(C12P17/10,C12R1:465),C12N15/00,C12N5/00
CC Mitomycin biosynthetic gene cluster
CC Mitomycin biosynthetic gene cluster
FH Key Location/Qualifiers
FT source I. .53500
/organism='Streptomyces lavendulae'.
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/organism='Streptomyces lavendulae''
/mol_type="genomic DNA"
/db_xref="taxon:1914"
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Unclassified.
1 (bases 1 to 53500)
2 Sherman, D.H., Mao,Y., Varoglu,M., He,M. and Sheldon,P. Sherman,D.H., Mao,Y., Varoglu,M., He,M. and Sheldon,P. Mitomycin biosynthetic gene cluster
Patent: US 6495348-A 76 17-DEC-2002;
Location/Qualifiers
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Pred. No. 17;
0; Mismatches 146;
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Sequence 76 from patent US 6495348.
AR266933

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AF127374 63734 bp DNA linear BCT 27-MAY-1999
Streptomyces lavendulae LinA homolog, cytochrome P450 hydroxylase
ORFA, cytochrome P450 hydroxylase ORF3, MitT (mitT), MitS (mitS),
MitR (mitR), MitL (mitD), MitR (mitE), MitO (mitO), MitN (mitN),
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MacA (mmcY), McC (mcY), MmcX (mmcX), and MmcY (mmcY) genes,
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Molecular characterization and analysis of the biosynthetic gene
cluster for the antitumor antibictic mitomycin C from Streptomyces
lavendulae NRRL 2564
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TGGACGAGGAAATCGAGCTGGTCCGCACCCCAAGCTGGACGAGGACATGAAGCGGC 331
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Mao, Y. Q., Varoglu, M. and Sherman, D. H.

Direct (Submission

Submitted (10-FEB-1999) Microbiology, Uni. of Minnesota, Box196, 420 Delaware St. St., Minneapolis, MN 55455, USA

Mao, Y. Q., Varoglu, M. and Sherman, D. H.

Direct Submission

Submitted (27-WAY-1999) Microbiology, Uni. of Minnesota, Box196, 420 Delaware St. St., Minneapolis, MN 55455, USA

Amino acid sequence updated by submitter

Location/Qualifiers
                                                                                                                                                                                            GCATCATCGCCCTAATCCTGGAGCGCCGTGAGCGCGGACAAGGCGGCGGCGATCGAGGA
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycincia, Streptomycetaceae, Streptomyces.
1 (bases 1 to 6)3734)
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CDS

CDS

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RDLGAAMAVQWPDAGTGTPVVVVTGAWLGAADALTFVLDSLVASVGSAPATRSAKALS
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function="putative regulator"
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/function="aminoDHQ synthase"
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Best Local Similarity 51.0%; Pred. No. 16;
Matches 152; Conservative 0; Mismatches
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'transī table=
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7895, 'RP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GWLLTRHADVRAALADPGVSSHPGKAPQPWRNLAPEWRABHYLPGFLIFMDPFDHTRY RRLEFR TEG VYFTLDAMENGGGTVOLVOSFALLF PELLVICELMG RRLETRWAIRKLEPRIEG VYFTLDAMENGGGTVOLVOSFALLFIPLINGLEBLMG RRYEREFROMVLRIQALDAT PEELCALGARMYERWKKLAAAKRANFGDDLLSHLAH DPDADPALTOLLEIGGGGVLMLIAGHESANMLGVGTYTLLENADQWALLRDDISLIDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVEELLRHOTIVQQGLPRGVTRDMEIAGHQVKTGESLLASLPAANRDPAVFPDPDRLD
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GSLVTARDEBDKLTRGELVRLARALI AGYETBASQI PRIEVYUTRHPDLLER RND
HDL IPDAVEELLRFYPIGTVDGFPRTATEDVELGGVLVRAGETVVPSKGAANRDPELF
TDPDELDLARRPNPHLGFGAGPHHCLGAQLARVELQITLTTEFRRYPRIRLAVPESSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILGELVQRVTGRSFRDFVTSELFAPLGLNDLHMGLPGSAWPRHVPARAAHPSEWPNQW
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GIDASLKRPVRWSHGFMLGGPGPDPRGLSNVLGRTSDPSAFGHAGTTSSVVWADPTRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORVTLPYGGEAMLATRYODVRAVFADRRFSRQLAVAPGAPRFLPHQPPPDAVLSVEGP
DHARLRRLVGKVFTPRRVEDMRPLIQRTADGLLDAMEEMGPPADLVEDFSLPFAVSMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVLAYLSNIQPEFGAGIERLREVSDLALGACEAG"
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/codon_start
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50316 CCGGCCGCGCCTCGCGGACCGGTGCGAGATCCTGCCCGGCGACTTCTTCGAGACCATCC 50375
                                                                                              50435
                                                                                                                                                                                        50436 TCGTACGCATCCTCCGCCGGATCGCCACCGCCATGAAGCCGGACTCCCGGCTCCTGGTCA 50495
                                                                                                                                                                                                                                                                                     50555
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AY310323 AY310323.1 GI:34766435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              He, J., Jeong, K.J., Lee, S.Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen, S., Huang, X., Zhou, X., He, J., Bai, L., Jeong, K.J., Lee, S.Y. and
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YTAPPRIDGLHPDLRTPTSLPPGRLNAELTEHLRALVAEHFPPFWAAKLLSTPAETTF
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LEGYHAARGPVGTAMVGLARRMGSAQVEETPDWSAMGQAEFDAWWQEQNNGSDRRSGF
                                                                                                                                              271
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                                                                                                                                                                                                                                                                                                                                                                               50556 TCGTCCTCGTCGCGCGCGCCCGAACGCTCGGAGAGCCGAATTCGCCGCCGCCTGCTGGAGAA 50613
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Huashan Road, Shanghai 200030,
                                                                                                                                                                                                                                                                                                                                  332 GCATCATCGCCCTAATCCTGGAGCGCCGTGAGCGCGACAAGGCGGCGGCGATCGAGGA 389
                                                 CCGACGACGCGGACCTCGTTGCCCGCGTCGCCCCAGGTGCTCGGCCTCGACCTCGACGAAG
                                                                                            212 CCCTCGCCGCCGCAGGTCTGCGCCCCCGGCGTCACCCCGGCCAGCGACCCAACCATGGACC
                                                                                                                                                                                                                                                                                  Octobrizational and Mutational Analysis of a Complete FR-008/Candicidin Gene Cluster Encoding a Structurally Related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces sp. FR-008
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _note="putative FAD-dependent monooxygenase"
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1 (bases 1 to 138203)
Chen,S., Huang,X., Zhou,X., Bai,L., He,J., Jeong,
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Direct Submission
Submitted (30-MAY-2003) Bio-X Life
Shanghai Jiaotong University, 1954
China
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1. .138203
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FR-008
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                                                 152
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VERSION
KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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JOURNAL
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COMPLEMENT (7210. .10254)
note="putative 4-amino-4-deoxychorismate lyase'
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/note="putative transcriptional regulator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="putative transcriptional activator"
/codon start=1
/roals_table=11
/producT="FSGRI"
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/gene="fscRIII"
/note="putative transcriptional regulator"
                                                                                                                                          /protein_id="AAQ82550.1"
/db_xref="GI:34766437"
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/db_xref="GI:34766438"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (4377. .7205)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (3150. .3818)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (4377. .7205)
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                                                                       /transl_table=11
/product="PabC"
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/trans[_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/transT_table=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="fscRI"
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gene

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ALQARKYRELEGVVDEVRPALMVVDCVAGFGVDLALARGIPYVLNVPFVASNVLTSHN
PFGASYTPKSFPVPNSGLPARNSVRQKLANTLFKWRTLGMFLHPDMAALLREDAAIRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /traislation="Marthpvsrpaldgreleyvsdavsggwissggpyvrrfeeafa
Ewngvahgvacssgtaaltilalralnigpgdevivpertmvasawavtytgatpvfvd
cgddinidvtrieekitprtravmpvhvygrrcdmdavmdlalqynlrvvedsaeahg
HLVPHR.PYAGTPPGATGPDGRRSAAPDL.PGTPRAHDAPRS.PGPEAAGRPDTAGPDEDP
AVAERHELTYJ.CRVASFLRHDDADL.DVLPVPAL.PDAVHRYAGVWAREHGVAGVHRE
EVRILARSEAVPAATGRFLLYVPRLLGCRALLILTDGDBEAENHIGALLDESHRERAAT
SVAHILTYRAELHI HEGRPDAAARDLAAAQAELPLDRLHPLFLPYWLALISMI TDLQVG
HTERARETAARPL.PPLAHESATTAQLLFARGVLARTDDEPHQAREHFRACGRWLLRHG
                                                                                                                                                                                                 CANDAVOPWRSIAAEAAHTLGDTEEAARLVHEEVRLARRWGAAAPLGRAQLSLAVVTE
ENRVENLRAAVTTLSAASARTAYTRAVIELAAAEREENERRTAVALGPAATVLPPVAP
PPGPHVPSAVARPPGPRPAVLTGRRTAKAPGHDAAVWHGLTAVERETAALAAQGLGNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSVTGGSFLEIVRLIRDIRSAGLGPDDTGTARLAQAGGKVVAASVRGVLEHQPDWVRQ
YARANVALGBERTYLAALGRVSVVHVREAVEIIRDAGLIHPGHLELSHBUTRAAVLD
VAGASGVAVLRRRAARLLSDVGRSPEIJATQLLLVPGTPDDWAVSVLRDAAQABQRG
ACEAAARYLERVREAEPKDPDVLSRLGKALAETDPARSVTLLHEAHSLTTDVRARAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVOLGLTCLAVQOSPDGARALTEALDALDAELGPEPEPADRELRTLTESALLIVGSDE
KATLPDILRRTEGLTPQPGDTPAQRQQLAMLSVLSAAEGGGAEETVGRARRALRAPGV
PLGVWSLLPTSLALSLADENEAAEEVLETVLRGSGDTAAVWTYVLALSTRSLFRLENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVPDAMADAQTALETIGGERWGDTATMPHTAYASVLTERGDPGRALEALDATKRPHLD
RFVWEYHWYLMARGRALAADGDLDGALOVFGSCGASMAEAGLTNPVLAPWLETACLL
GEAGRGEEAGRAAAHGTRLAERWGTRRALGYAALARGAAARGTARTGALREAVALLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPARGGHARGILLLGRALVEDGAVREGREHLREAVGLARRCGCVALARRARDEL IAAG
GRMREVTASPLDMLTGTERTVAGLVASGAGNREVAESLFVTVRTVELHLTSVYRKLGV
ARRGDLTEALREAGATARPAAERRPGHAKRRNP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELGT APPNAWTRVDERAAVVCSSVAELDYPFOI PDRVSLVGAVLPPLPFAPDDDEVTR
WLDAQSSVVXMGFGTI TRLTREEVAALVEVARRMSGTHQFLWKLPKEQQHLLPBAGSL
PDNLRVESWVPSQLDVLAHPNVSVFPSHGGGNAYHEGVYFGKPQVVRPLWVDCFDQAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRPVGDIACFSLFANKIITAGEGGVCLTDDPRLAEQLAHLRAWÄFTRDHSFLHKKLAY
NYRWTAMQGAVALAQTERLDEILATRREIEARYDAGLKDLPGITLMPARDVLWMYDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPGSTFSVLQGLYWLAANLMADGPLVLVLDDVHWCDSRSLRWLDFLLRRADGLPLLVV
AAHRTGTGLTAPDALADLVAHHLPASLGLGPLDTAEVAELTAHSFPEQDPLPSFVGRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGRDFGISLTLDKPHTVDPDDVVDKLTRVTSDPAFRTBAERLGALQRAAGGRAAAADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MWLRWACDRSRGAAPGRSGSAGPPSLAPSDARESPVPHRSRAVP
PAPPLVGRAHQLDVLARHADAARAGRPRLVLLDGPAGIGKTALLRAALAEDGPLAGMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLYGSCRAVDVATGYSGVRALFGGLGLTGRKGRTSPLLVGGARRALPALAADPGELDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="putative aminotransferase responsible for
                                                                                                                                                                                                                                                                                                                EIATELAVTTRAVELRLSGVYRKLRIRGREELRALVQEAEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="putative transcriptional regulator"
                                                                                                                                                                                                                                                                                                                                                                 complement (10298. .13315)
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/db_xref="GI:34766443"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              id="AAQ82554.1"
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/db_xref="GI:34766442"
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/db_xref="GI:34766441"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="FscRIV"
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/transl_table=11
/product="FscMI"
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/gene="fscMII"
14953. .16011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
/transl_table=1
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/gene="fscMI"
13522. .14898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="fscRIV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="fscMII"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (20-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The following sequence is oriented from the T7 to the SP6 end. Upstream BAC (overlapping the T7 end) : OSJNBa0031E02 (AC=AL954632)
AERREELRAHLDARGI ETRL FFXPMSRQPGYLDPVWPTLNAHRFSEDGLYLPTHTGLT
                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa, (japonica cultivar-group)
Sukaryota, Virtálplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGACGGCAAGAACCGGCCCGACGACGACGACCTCGTTGCCCGGCGTCGCCCAGGTGCTC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCCTCGACCTCGACGAAGCCCTCGCCGCCGCAGGTCTGCGCCCCCGGCGTCACCCCGGCCA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 GCGACCCCAACCATGGACCTGGACGAAATCGAGCTGGTCCGCACCGACCCCAAGCTG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGACCAAGAGCGAGTTGGCCAGGCGCATCCAGAAGGACCGGGCCACCGTCGGCCGGTGG 132
                                                                                                                                                                                                                                                                                  Gaps
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Choisne, N., Orjeda, G., Cattolico, L., Demange, N., Wincker, P., Sequens, B., Pelletier, E., Scarpelli, C., Salanoubat, M., Wissenbach, J. and Quetier, F. Oryza sativa chromosome 12 sequencing Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Nov 9, 2002 this sequence version replaced gi:23477037.
Center: Genoscope / Centre National de Sequencage
Center code: GS
                                                                                                                  Length 138203;
                                                                                                                                                                                                      6
                                                                                                                                                                                                      Indels
                                                                                                                                                            Pred. No. 13;
0; Mismatches 166;
                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.genoscope.cns.fr/
Contact: SegRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCTTCTCCTCGATGTCCGGCATCCTCGGC 56199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACGAGGACATGAAGCGGCGCATCATCGCC 342
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FINISHED SEGMENT ENDS AT BASE 145539
                                                                                                                          Score 64.4;
Pred. No. 13
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                                                                                                                      Udery Match
Best Local Similarity 49.7%;
Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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VERSION
KEYWORDS
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AUTHORS
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JOURNAL
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TITLE
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/organism="Oryza sativa (japonica cultivar-group)"

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                                                                                                                                                                                                                                                                                                                                         34685 GCAGCCAGAGCTACGTGCTCACCAAGGGCTGGAGCCGCTACGTCAAGGAGAAGCGCCTCG 34744
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Beniley.S.D.

Direct Submission

Submitted (09-MAY-2002) Submitted on behalf of the Streptomyces sequencing team, Sanger Institute, Wellcome Turus Genome Campus, Hinxton, Cambridge (1810 18A E-mail: schosesnger.ac.uk on or before Oct 30, 2002 this sequence version replaced gi:4500374; gi:4990618, gi:499078, gi:6138834, gi:75242, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276800 bp DNA linear BCT 11-FEB Streptomyces coelicolor A3(2) complete genome; segment 12/29. A1939115 AL035640 AL035554 AL035707 AL049573 AL132674 AL354048 AL355832 AL35989 AL442120 AL596138 AL645882
                                                                                                                                                                                                                                                                                                GCATCCAGAAGGACCGGCCACCGTCGGCCGGTGGGAGGACGGCAAGAACCGGCCCGACG
                                                                                                                                                                                                                                                                                                                                                                                         158 ACGCGGACCTCGTTGCCCCGCGTCGCCCCAGGTGCTCGGCCTCGACGACGAAGCCCTCG
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Streptcomyces coelicolor A3(2)
Bacteria; Actinobacteria; Actinobacteridae, Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                         Length 145539;
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48...98
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                                                                                                                                                                                                         DB 8;
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55.8%; Pred. No. 16;
ive 0; Mismatches
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                                                                                                                                                                                                                                                       Matches 121; Conservative
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/db xref="SP
                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein, len:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aa: similar to many in Streptomyces coelicolor eg.
TR:09F3E9 (EMBL:AL450289) SC2H2.06 hypothetical protein
[150 aa) fasta scores; opt: 340, Z-score: 415.4, 46.032$
sidentity in 126 aa overlap and upstream neighbouring CDS
SCBAC19G2.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1558..2688)
/gene="SCO3057"
/note="SCBAC19G2.12c, possible dipeptidase, len: 376 aa:
                                                                                                                                                                                                                                                                         /gene="SCO3054" '026',
/gene="SCO3054" '026',
/noce="SCBAC1962.09c, conserved hypothetical protein, ler
168as similar to many in Streptomyces coelicolor eg.
TR:09F2X0 (EMBL:AL192148) SCD20.09 hypothetical protein
(190 aa) fasta scores; opt: 250, Z-score: 285.6, 34.503%
identity (38.816% ungapped) in 171 aa overlap."
/codon start=1
                                                                                   gaps"
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complement(146. .652)
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/gene="SCO3056"
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/note="SCBAC19G2.13c, possible dipeptidase, len: 400 aa: similar to many eukaryotic peptidases e.g. SW:331429 (MDP1 RABIT) rabbit renal dipeptidase (410 aa) fasta scores; opt: 788, Z-score: 879.1, 42.43% identity (48.580% ungapped) in 403 aa overlap. Also weakly similar to TR:09KH70 (EMBL:AF268476) thermostable dipeptidase from Brevibacillus borstelensis (307 aa) fasta scores; opt: 450, Z-score: 506.1, 31.034% identity (36.486% ungapped) in 348 aa overlap. Contains Pfam match to entry PF01244 Renal dipeptiase, Renal dipeptidase, Also similar to neighbouring downstream CDS SCBAC19G2.12c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LARAHAVLAAHPVADGCNGLPWALRHLPWYDLEIGESAVDTDVPRLREGHVGALLWSL
HALPESLDGDRAVGATLEQLDLVKTVVRAHPEGLRLAYDAGQAIDARNCGRIAVDEGPA
GAAALGDRLGILRSLHALGLGLVLTLSGVSWASEAGLTRFGEEVVREMRLGVVADLSG
ASAETVRRTRAVSKAPALCTRGAARALRPHPANLPDDLLVBLGAAGGLCWVPLTARGT
GPTVRDVADHLDHVRTVAGPQSVGLSGTYDSGAAHPLEIGDPSCYPRLVAELIRRGWD
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COMPLHENT (1561 . 2616)
                                                                                                                                                                                                                                                                                                                                                                                                       /transI_table=11
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/tb_xref="NPTRMBL:093146"
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CDHPRNI PDDVLERLSANGGMAMVTFVPKFVLQAAVDWTAEADDNWRAHGFHHLDSSP
EAMKVHAAFEERVPRPVATVSTVADHLDHMREVAGVDHLGI GGDYDGTPFTPDGLGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /iote="Pfam match to entry PF01244 Renal dipeptase, Renal dipeptidase, score 121.70, E-value 1.4e-32" complement (1562. 2643) / inte="Degenerately, directly repeated at 13490. .14610" / gene="SC03058" 4010)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGYPNLIAELLDRGWSQSDLAKLTWKNAVRVLDAAEDVSRGLRAARGPSNATIEQLDG
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similar to many eukaryotic peptidases e.g. SW:P31430 (MDP1_RAT) rat renal dipeptidase (410 aa) fasta scores; opt: 440, Z-score: 474.0, 36.056$ identity (38.906$ ungapped) in 355 aa overlap. Also weakly similar to TR:Q9KH70 (EMBL.AF268476) thermostable dipeptidase from Brevibacillus borstelensis (307 aa) fasta scores; opt: 273, Z-score: 289.4, 28.159$ identity (30.116$ ungapped) in 277 aa overlap. Contains Péam match to entry PF01244 Renal dipeptiase, Renal dipeptidase. Also similar to heighbouring upstream CDS SCBAC19G2.13c"
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complement (4025. .4567)
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/gene="SCO3058"
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/EC number="4.1.1.21"
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CDS

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/note="SCBAC19G2.14c, phosphoribosylaminoimidazole carboxylase catalytic subunit PurE, len: 180aa: strongly similar to many eq. Sw:Q44679 (PURG_CORAM) phosphoribosylaminoimidazole carboxylase catalytic subunit PurE from Corynebacterium ammoniagenes (177 aa) fasta scores; opt: 666, Z-score: 735,8,65,541% identity (65.24% ungapped) in 148 aa overlap and TR:080937 (EMBi:AC04684) putative phosphoribosylaminoimidazole carboxylase from Arabidopsis thaliana (645 aa) fasta scores; opt: 644, Z-score: 703.2, 60.870% identity (60.870% ungapped) in 161 aa overlap. Contains Pfam match to entry PR0731 AIRC, AIR carboxylase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGCGTCGAGAAGGCCGTGCTGGCCGTCATCGAGCAGATCGGCCCGGAGCTGGGTCGGCTA 43377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 CATGGACCTGGACGAGGAAATCGAGCTGGTCCGCACCCCCAAGCTGGACGAGGACAT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perez Pons, J.A., Cayetano, A., Rebordosa, X., Lloberas, J., Guasch, A. and Querol, B.
A beta-glucosidase gene (bgl3) from Streptomyces sp. strain QM-B814. Molecular cloning, nucleotide sequence, purification and characterization of the encoded enzyme, a new member of family 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 GCGCGGCACATGGGCCGCATACGTCCTCACCGCCCGCGAGCGCGGCGGACTGACCAAGAG 83
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Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 2081)
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                                                                                                                                                                                                                                                                                                                                                                           Score 62.6; DB 1; Length 2. Pred. No. 17; 0; Mismatches 164; Indels
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Eur. J. Biochem. 223 (2), 557-565 (1994)
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161; Conservative (
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ALRDALGDRYKTWYTINILABPWCSAFLGYGSGYHAPGRATDDYAALRAHHIMIGHGIAVO
ALRDRLPADAQCSVTLNIHHVRPLTDSEADADAVRRIDALANRVFTGPMLGGAYPEDL
VRYTAGLIFUMGSFYRDGDIEKLAHGKOLDFGWYNYSPTIVUSEADGSGYHNBOGARPEDL
VRYTAGLIFUMGSFYRDGDIEKLAHGKOLDFGWYNYSPTIVUSEADGSGYHNBOGARFHDYA
DPEGNYNDPERIAPGRAYUPSGILYELLRRLSSDFPALPLYUTENGAFHDYA
DPEGNYNDPERIAYRGYBHYARGYBYRGYBYA
1676. . 1719
/note="Putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xxef="GOA:QS9976"
/db_xxef="SPTREMBL:QS9976"
/db_xxef="SPTREMBL:QS9976"
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/translation="MVPAAQQTATAPATHRWREDVALMAELGLGAYRFSLAWPR:QPTGR
GPALQKGLDFYRRLADELLAKGIQPVATLYHWDLPQELENPGGWPERPTAERFAEVAA
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                                                                                              /EC number="3.2.1.21"
/function="hydrolyzes cellobiose and other
beta-D-glucosides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.5%; Score 61.6; DB 1; 50.0%; Pred. No. 89; ive 0; Mismatches 154;
                              /mol_type="genomic DNA"
/strain="QM-B814 (ATCC 11238)"
/db_xref="taxon:1931"
/clone="Clone pJC911"
                    organism="Streptomyces sp."
                                                                                                                                                                                                                                                                                                                                                                                  /product="beta-glucosidase"
/protein_id="CAA82733.1"
/db_xref="GI:581738"
                                                                                                                                                                                                                                                                                                                                          codon_start=1/evidence=experimental
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                                                                                                                                                                                                                            gene="bgl3"
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/gene="bgl3"
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RESULT 15 BD179992

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BDI/9992 1233 bp DNA linear PAT 15-MAY-2003
Highly thermophilic bacterium-deriyed protein and gene encoding it.
BDI/9992
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NARUKI KURAMITSU, SHIGEYUKI YOKOYAWA
C12N15/09,C12N15/09,C07K14/195,C12N1/15,C12N1/19,C12N1/21, PC
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Highly thermophilic bacterium-derived protein and gene CC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kuramitsu, N. and Yokoyama, S.
Highly thermophil. C bacterium-derived protein ar Patent: JP 200235574-A 483 12-NOV-2002;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH OS Thermus thermophilus PN JP 2002325574-A/483
PD 12-NOV-2002
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Coganisme="Thermus thermophilus"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## SUMMARIES

110 110 110 110 110 110 110 110	SUMMAKIES	Description	Aad25932 Micromono	1 Aas08694 Micromono	Aag12342 Actinomyc	ω,	l Adel0251 S. lavend	Aac55842 Complete	l Adel0261 S. lavend	l Aaa58471 Nucleotid	Abz66792 Orthosomy	Abz66808		Adc08080 Rice	Aad54645	Aaf12486	Aa140781	Aal61172 Actinosyn	4 Aal61224 Actinosyn	3 Abz71158 S. muraya	l Abz71131 Streptomy	5 Aca03525 Synthetic	Acc78498	8 Ada70128 Rice gene	
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11.05.6 11.05.		Score	426	426	99	64.4	64.4	64.4	64.4	9.09	56.8	56.8	56.2	56.2	56.2	56	55.4	55	. 25	54.2	54.2	53.8	ო		
Match Match		Result No.		7	m	4	'n	φ	7	60	o	10	11	12	13	14	15	16	c 17	18	c 19		21	22	

Abs78655 S. macrom	Aca42530 Prokaryot	Aav26609 Actinomad	Aas08693 Micromono	Aad17186 Streptomy	Aad36874 Streptomy	0	Abz58812 S. cinnam	Ada71938 Rice gene	Aad17185 Streptomy	Aca03527 Synthetic		Ada71184 Rice gene	Aca37879 Prokaryot	Aat80414 Platenoli	Aat78508 Platenoli	Aca37764 Prokaryot	Aadl7184 Streptomy	Abz66673 Orthosomy	Aca37577 Prokaryot	Aac55788 Hydroxyla	Adel0207 S. lavend
ABS78655	ACA42530	2 AAV26609	. AAS08693	4 AAD17186	, AAD36874	ADA69780	, ABZ58812	ADA71938	AAD17185	, ACA03527	ADC13260	, ADA71184	, ACA37879	AAT80414	: AAT78508	ACA37764	4 AAD17184	/ ABZ66673	7 ACA37577	1 AAC55788	ADE10207
5811 6	1266 7		109519 5	•	29870 7	1185 7	17083 7	2000	27541 4	861 7	861 9	1389 7	1527 7	44377 2	44377 2	543	40	1047	٠	1224 3	1224 9
12.4	12.4	12.4	12.4	12.3	12.2	12.1	12.1	12.1	12.1	12.0	12.0	12.0	12.0	12.0	12.0	11.9	11.9	11.9	11.9	11.8	11.8
53	52.8	52.8	52.8	52.4	52	51.6	51.6	51.4	51.4	51.2	51.2	51.2	51	51	51	50.8	50.8	50.6	50.6	50.4	50.4
24	25	26	27	28	29	30	31		33	34		36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

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Integrase, int, excisionase, xis, integrase attachment site, attP, pMLP1, site-specific integration; hybrid antibiotic, metabolic product; secondary metabolic pathway; ds.
                                                                                                                                                                                                                                                                                            Novel polynucleotides encoding integrase, excisionase and an integrase attachment site isolated from a lysogenic phage pMLP1, useful for transforming an actinomycete.
                                                                 Micromonospora carbonacea pMLP1 excisionase DNA
      AAD25932 standard; DNA; 426 BP.
                                                                                                                                                                                          15-MAY-2001; 2001WO-US015760.
                                                                                                                                                                                                               17-MAY-2000; 2000US-0204670P.
                                              (first entry)
                                                                                                                              Micromonospora carbonacea.
                                                                                                                                                                                                                                 (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                      Hosted TJ, Horan AC;
                                                                                                                                                                                                                                                                          WPI; 2002-082983/11.
                                                                                                                                                  WO200187936-A2.
                                               26-MAR-2002
                                                                                                                                                                      22-NOV-2001.
                           AAD25932;
AAD25932
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Claim 5; Page 32-33; 34pp; English

The present invention relates to novel polymucleotides encoding integrase (int) and excisionase (xis) and an integrase attachment site (atta) which are isolated from pMLP1, a bacteriophage (lysogenic phage) isolated from Micromonospora carbonaca var. africana. Polymucleotides of the invention are useful for transforming an actinomycete with a vector. They are also chromosomes. The integrating vectors are used to express actinomycete penes, manipulate secondary metabolic pathways and create new metabolic products such as hybrid antibiotics. The present sequence is pMLP1 excisionase DNA from Micromonospora carbonacea

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Local Sim
es 426;
                                                                                                                                                Hosted TJ,
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The sequence encodes 2 integrases which permit site specific integration of a vector into an actinomycete, especially a Micromonospera, genome. The invention relates to nucleat acids and vectors comprising a M. carbonacea everninomicin biosynthetic pathway resistance gene product carbonacea everninomicin bathway gene the vector is useful for introducing a m. continue for the vector is useful for introducing a certain of the vector is useful for introducing a certain for the genus Micromonospora. The DNA encoding the biosynthetic proteins is consetul for synthesising novel everninomicin-related compounds, arising from modifications of the DNA sequence designed to change glycosyl and modified orsellinic acid groups contained in everninomicin, for modified orsellinic acid groups contained in everninomicin, for complete or much control or mutant everninomicin blosynthetic enzyme for evaluation, diagnosis and preferably biosynthesis of everninomicin or cother secondary metabolic products, improving the yield of everninomicins and preferably biosynthesis of everninomicins and contains and also as a hybridisation probe to combinatorial biosynthesis. The encoded polypeptides are useful for combinatorial biosynthesis to generate libraries of orthomycins, e.g. the integrase allows flow increased by products and drug discovery. The bnA encoded products cortain analogues/homologues and drug discovery. The bnA encoding the integrase the yield of known products or to generate genes of choice into chromosomes of different hosts and to integrate genes. The vector can also be used to increasing a given gene dosage. The integrate contains and to integrate and to prementation processes involving to early out bioconversions with compounds to which the strain is containly sensitive and is thus useful in fermentation processes involving engine e.g. Streptomyces antibioticus. (Updated on 11-SBP-2003 to standardise of e.g. Streptomyces antibioticus. (Updated on 11-SBP-2003 to standardise on the products and seed to integrate endormall
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecules encoding everninomicin pathway gene useful for improving yields of everninomicin, to produce new everninomicin and as probes to identify homologous sequences.
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                                                                                                                                                                                                                                                                                           Wang TX;
12-JAN-2001; 2001WO-US001187.
                                                                                            12-JAN-2000; 2000US-0175751P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acid molecule comprising mitomycin biosynthetic gene cluster useful for cloning mitomycin biosynthetic genes for elucidating the molecular basis of mitosane ring system biosynthesis.
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                                                                                                                                                                                                                                               886 cascassicarcas de casas de contra de la casa de ca
                                                                                                                                                                                                                                                                                                                                                                                                                  307 AAGCTGGACGAGGACATGAAGCGGCGCATCATCGCCCTAATCCTGGAGCGCCGTGAGCGC
                                         GOCCOCTCAACCACACCGAGGGCGCCGAACCACCTGGTCGGCCCGTCAGCCGCCGCC
                                                                                                     CGGTGGGAGGACGGCAAGAACCGGCCCCGACGCGCGCGCCTCGTTGCCCCGCGTCGCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S. lavendulae MmcR encoding DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCAACTCCGTGATGATC 1023
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P-PSDB; AAB32531.
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VAROGLU M.
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(ASAH ) ASAHI KASEI KOGYO KK
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P-PSDB; AAR12786
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25-MAR-2003
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mitomycin biosynthetic gene cluster comprises 47 mitomycin genes spanning 55kb of DNA. The invention includes an expression cassette comprising a mitomycin biosynthetic gene operably linked to a promoter, and host cells transformed with the cassette. The nucleotide, and protein sequences and the transformed with the cassette. The nucleotide and protein sequences and cativities. The nucleotide sequenced in antiasthmatic, antiinflammatory, cytostatic, immunomodulatory, and antibiotic cativities. The nucleotide sequence are used to elucidate the molecular basis for the biosynthesis of the mitosane ring system, as well as to engineer the biosynthesis of novel natural products, e.g. antibiotics, anti-inflammatory agents, anti-cancer agents, immune-enhancers, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other disease involving respiratory inflammation, or cholesterol-lowering agents or as crop protection agents (e.g. fungicides or insecticides) as well as bipolymers, e.g., in packaging or biomedical applications, or to engineer PRA monomer synthases. Sequences AAG55782-C558814, AAG58815-C55885 and AAB32485-B32542 represent mitomycon biosynthetic gene cluster DNA sequences and encoded proteins. Sequences AAG55812-C55814 AAG5880-C55886 and AAG58862-C55889 represent PCR
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    lavendulae mitomycin biosynthetic protein MmcR gene.

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Best Local Similarity 51.0%;
Matches 152; Conservative
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(MAOY/) MAO Y.
(VARO/) VAROGLU M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2003134398-A1.
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The invention relates to an isolated and purified nucleic acid molecule comprising a sequence having mitomycin biosynthetic gene cluster, or its variant or fragment. Also included are an expression casester comprising the novel nucleic acid molecule (operably liked to a promoter functional in a host cell), a recombinant bacterial host cell in which at least a preter and uncleic acid molecule comprising mitomycin biosynthetic gene cluster is disrupted (resulting in a recombinant host cell) that produces altered levels of mitomycin relative to a corresponding nonrecombinant bacterial host cell), introducing exogenous DNA into a refractory streptomycin strain, identifying a nucleic acid molecule that is related to at least a portion of a nucleic acid molecule comprising a mitomycin cell and a product produced by the recombinant host cell. The nucleic acid encodes a Mitt, M
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                                                                                                                                                                                                                                                                                                              New nucleic acid molecule comprising a sequence having mitomycin biosynthetic gene cluster, useful for enhancing production of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1056 BP; 152 A; 427 C; 338 G; 139 T; 0 U; 0 Other;
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                                                                                                                   Sheldon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 66; 308pp; English.
                                                                                                              He M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC55842 standard; DNA; 53500 BP
                                                                                                                   Varoglu M,
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152; Conservative
                                                                                                              Sherman DH, Mao Y,
                                                                                                                                                                                               2003-863498/80.
                                      SHELDON P.
                                                                                                                                                                                                    WPI; 2003-863498
P-PSDB; ADE10303
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This invention relates to isolated and purified nucleic acid molecules from the mitomycin biosynthetic gene cluster. Mitomycins are a group of natural products that contain a variety of functional groups, including amino benzoquinone and axidine ring systems. The S. lavendulae can incomycin biosynthetic gene cluster comprises 47 mitomycin genes spanning 55kb of DNA. The invention includes an expression cassette comprising a mitomycin biosynthetic gene poerably linked to a promoter, and host cells of transformed with the cassette. The nucleotide, and protein sequences and the transformed with the cassette. The nucleotide, and antibiotic antiinflammatory, cytostatic, immunomodulatory, and antibiotic antiinflammatory diversatic, immunomodulatory, e.g. antibiotic activities. The nucleotide sequences are used to elucidate the molecular basis for the biosynthesis of the mitosane ring system, as well as to engineer the biosynthesis of novel natural products, e.g. antibiotics, anti-inflammatory agents income agents, immune-enhancers, immunosuppressants, agents to treat asthma. chronic obstructive pulmonary disease as well as other disease involving respiratory inflammation, or cholesterol-lowering agents or as crop protection agents (e.g. fungicides or insecticides) as well as bipolymers, e.g., in packaging or biomedical applications, or to engineer PRA monomer synthases. Sequences AACSSRSC-CSSRSQ and AACSSRSC-CSSRSG prepresent mitomycin biosynthetic genes Custer DNA sequences and encoded proteins. Sequences AACSSRSC-CSSRSG and AACSSRSC-CSSRSG prepresent por protein genes cluster DNA sequences and encoded proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acid molecule comprising mitomycin biosynthetic gene cluster useful for cloning mitomycin biosynthetic genes for elucidating the molecular basis of mitosane ring system biosynthesis.
        antibiotic; anti-cancer;
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Mitomycin, biosynthesis, mitosane ring system, antibiotic, anti-
anti-inflammatory, immune-enhancer; immunosuppressant, asthma;
chronic obstructive pulmonary disease; respiratory inflammation;
fungicide; pesticide; ds.
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                                                                                                                                                                                                  Streptomyces lavendulae.
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Best Local Similarity
Matches 152, Conservat
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(SHEL/)
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The invention relates to an isolated and purified nucleic acid molecule comprising a sequence having mitomycin biosynthetic gene cluster, or its variant or fragment. Also included are an expression cassette comprising the novel nucleic acid molecule (operably linked to a promoter functional in a host cell), a recombinant bacterial host cell in which at least a portion of a nucleic acid molecule comprising mitomycin biosynthetic gene cluster is disrupted (resulting in a recombinant host cell that produces altered levels of mitomycin relative to a corresponding nonrecombinant bacterial host cell), introducing exagenous DNA into a refractory streptomycin strain, identifying a nucleic acid molecule that is related to at least a portion of a nucleic acid molecule comprising a mitomycin of a nucleic acid molecule comprising a mitomycin cell and a product produced by the recombinant host cell and a product produced by the recombinant host cell and a product produced by the recombinant host cell and a product produced by the recombinant host cell and a product produced by the recombinant host cell and a product produced by the recombinant host cell and a product produced by the recombinant host cell and a product produced by the recombinant host cell and a product produced by the recombinant host cell and a product produced by the recombinant host cell and a product produced by the recombinant host cell and a product produced by the factor of acid is useful for enhancing production of mitomycin antibiotics, which induce apoptosis and hence are useful as anti-tumour (via tumour hypoxia) agents and are useful in treating cancer. The agene cluster was isolated from Streptomyces lavendulae. The present sequence is an operon or gene cluster encoding the mitomycin biosynthetic proteins of the invention.
                                        43696 icgácaaccicardadagagagacacadadagaacartaakagataticardadagaatagaga 43755
                                                                                                                                       43756 TÖGTÖCTÖGTÖGCGGÖGCCGAACGÖTGGAAGGÖAATTOGÜGGCGCTGCTGGAGAA 43813
TGGACGAGGAAATCGAGCTGGTCCGCACCGAACCCCAAGCTGGACGAGGACATGAAGCGGC 331
                                                                                            GCATCATCGCCCTAATCCTGGAGCGCCGTGAGCGCGACAAGGCGGCGGCGATCGAGGA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitomycin biosynthetic protein; mitomycin C; antibiotic; MC; apoptosis; tumour hypoxia; cytostatic; anti-tumour agent; cancer; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New mucleic acid molecule comprising a sequence having mitomycin biosynthetic gene cluster, useful for enhancing production of antibiotics.
                                                                                                                                                                                                                                                                                                                                                                                                   S. lavendulae mitomycin biosynthetic genes complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces lavendulae.
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VAROGLU M.
HE M.
SHELDON P.
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P-PSDB; AAB07556, AAB07557, AAB07558, AAB07559, AAB07560, AAB07561, AAB07562, AAB07562, AAB07563, AAB07564, AAB07565, AAB07566, AAB07569, AAB07569, AAB07576, AAB07576, AAB07577, AAB07578, AAB07576, AAB07577, AAB07578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New bleomycin gene cluster components useful for peptide and/or polyketide metabolites, especially bleomycin, production and for
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/note= "ORF 9; encodes AAB07577"
57583. .58857
                                                                                             *tag= 1
frams1_except= (pos: 1..3, aa: Met)
note= "ORF 19; encodes AAB07567"
7299. .39215
                                                                                                                                                                                                                                                                                    transl except= (pos: 1. .3, aa: Met)
note= "ORF 15; encodes AAB07571"
0998. .52386
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"ORF 10; encodes AAB07576"
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*note= TORF 20; encodes AAB07566"
$818. .37302
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Transl_except= (pos: 1. .3, aa: N
Trote= "ORF 18; encodes AAB07568"
9301. .47181
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note= "ORF 17; encodes AAB07569"
7178. .49985
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note= "ORF 13; encodes AAB07573".
3018. .54190
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note= "ORF 12; encodes AAB07574"
4187. ,55824
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note= "ORF 11; encodes AAB07575"
5821. .56093
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hote= "ORF 21; encodes AAB07565"
4827. .35804
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note= "ORF 8; encodes AAB07578"
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56090. .57586
2893. .34830
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05-FEB-1999; 99US-0118848P.
05-JAN-2000; 2000US-00477962.
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2383.
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                                                                                              CCGACGACGCGGACCTCGTTGCCCGCGTCGCCCAGGTGCTCGGCCTCGACCAAG 211
                                                                                                                                            CCCTCGCCGCCGCAGGTCTGCGCCCCGGGTCACCCCGCCAGCGACCCAACCATGGACC 271
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                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     BLM gene cluster; bleomycin gene cluster; polyketide metabolite;
bleomycin; bleomycin analogue; holo-carrier protein; thiazolidine;
thiazoline; bithiazoline; microbial metabolite; sugar; ss.
                                                                                                                                                                                                                                                                                                                                                                                               Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 8-30.
 Query Match 15.1%; Score 64.4; DB 9; Length 53500; Best Local Similarity 51.0%; Pred. No. 0.0091; Matches 152; Conservative 0; Mismatches 146; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transl except= (pos: 1. .3, aa: Met)
note= "ORF 27; encodes AAB07559"
806. .12294
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note= "ORF 23; encodes AAB07563"
4663. .32690
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transl_except= (pos: 1. .3, aa: Met)
note= "ORF 30; encodes AAB07556"
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/transl_except= (pos: 1. .3, aa: Met)
/note= "ORF 29; encodes AAB07557"
2767. .3486
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note= "ORF 24; encodes AAB07562"
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note= "ORF 25; encodes AAB07561"
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/note= "ORF 22; encodes AAB07564"
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1527. .5593
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note= "ORF 26; encodes AAB07560"
2291. .15491
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                                                                                                                                                                                                                                                                                                                                    91 GCCAGGCGCATCCAGAAGGACCGGGCCACCGTCGGCCGGTGGGAGGACGGCAAGAACCGG 150
                                                        The present sequence represents the BLM (Bleomycin) gene cluster, containing open reading frames (ORFS) 8-30. The proteins encoded by the gene cluster are useful for producing peptides and/or polyketide metabolites, especially bleomycin or bleomycin analogues. They are also useful for chemically bleomycin or bleomycin analogues. They are also useful for chemically modifying biological molecules to produce branched methyl groups, and for coupling amino acids and fatty acids. They may be reacted with an apo-carrier protein and coenzyme A to produce a holocarrier protein. The BLM gene cluster or catalytic domains can be used hithiatuly or collectively to produce thiazolidine, thiazoline, bithiazoline and bithiazoline-containing microbial metabolites. The BLM gene cluster may also be used to produce sugars
                                                                                                                                                                                                                                                                                                                                                                   151 CCCGACGACGCGGACCTCGTTGCCCGCGTCGCCCAGGTGCTCGGCCTCGACCTCGACGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 GCCCTCGCCGCCGCAGGTCTGCGCCCCCGGCGTCACCCCGGCCAGCGACCCCAACCATGGAC
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14.2%; Score 60.6; DB 3; Length 58857;
Best Local Similarity 49.5%; Pred. No. 0.041;
Matches 156; Conservative 0; Mismatches 159; Indels 0;
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 chemically modifying biological molecules.
                                Claim 8; Page 97-136; 162pp; English
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30-MAR-2001; 2001US-0279709P.
20-APR-2001; 2001US-0285214P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to identifying orthosomycin biosynthetic genes and its fragment/gene cluster (ABZ66670-ABZ66813), comprising detecting the presence of a nucleic acid sequence coding for a polypeptide (ABP99207-ABP9952). The method is useful for identifying an orthosomycin biosynthetic gene, gene fragment or gene cluster, especially an eventinomicin-type or avilamycin-type orthosomycin biosynthetic gene, gene fragment or gene cluster. The method is useful for detecting the presence of any organism that contains DNA for the production of orthosomycins regardless of the level at which genes for orthosomycin production are expressed by the organism or the amount of orthosomycin produced by the organism. This allows for the detection of new
                                                                                                                                                                                                                                      Identifying orthosomycin biosynthetic gene, gene fragment or gene cluster, by detecting presence of nucleic acid sequence corresponding 17 of flambamycins protein families.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 GGCCACCGTCGGCCGGTGGAGGACGGCAAAAACCGGCCCGACGACGGGACCTCGTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
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Pred. No. 0.27;
0; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   orthosomycin natural products, not produced by the organism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGCACCGACCCCAAGCTGGACGAGACATGAAGCGGCGC 333
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Staffa A;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 29; Page 397; 511pp; English.
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30-MAR-2001; 2001US-0279709P.
20-APR-2001; 2001US-0285214P.
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Best Local Similarity 53.6%;
Matches 118; Conservative 0
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Zazopoulos E,
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                                                                                              WPI; 2003-058435/05.
                                                                                                                                             P-PSDB; ABP99329
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Chang H, Ch
Katagiri F,
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                                                                                                                        The invention relates to identifying orthosomycin biosynthetic genes and its fragment/gene cluster (ABZ66670-ABZ666813), comprising detecting the presence of a nucleic acid sequence coding for a polypeptide (ABB99207-ABP99362). The method is useful for identifying an orthosomycin biosynthetic gene, gene fragment or gene cluster, especially an everninomicin-type or avilamycin-type orthosomycin biosynthetic gene, gene fragment or gene cluster or denecting the presence of any organism that contains DNA for the production of orthosomycins (both everninomicin-type orthosomycins and avilamycin-type orthosomycins and avilamycin-type orthosomycins) regardless of the level at which genes for orthosomycin production are expressed by the organism or the amount of orthosomycin produced by the organism. This allows for the detection of new orthosomycin natural products, not produced by the organism
                                                                                                                                                                                                                                                                                                                                                               173
                                                                                                                                                                                                                                                                                                                                                                                                            233
                                                                                                                                                                                                                                                                                                                                                                                                                                                        293
                                                       Identifying orthosomycin biosynthetic gene, gene fragment or gene cluster, by detecting presence of nucleic acid sequence corresponding to 17 of flambamycins protein families.
                                                                                                                                                                                                                                                                                                                                                                                    CCGCGTCGCCCAGGTGCTCGGCCTCGACCTCGAAGCCCTCGCCGCCGCGCAGGTCTGCG
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                                                                                                                                                                                                                                                                                                                  Length 45055;
                                                                                                                                                                                                                                                                                                               13.3%; Score 56.8; DB 7; Length 4 53.6%; Pred. No. 0.19; or Mismatches 102; Indels
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                                                                                                      Example 2; Page 425-450; 511pp; English,
             Staffa A;
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                                                                                                                                                                                                                                                                                                                             Local Similarity 53.6
nes 118; Conservative
             Zazopoulos
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                                  WPI; 2003-058435/05
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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance to a plant to bacterial, fungal or viral infection. The present sequence was used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72
                                                                                                                                                                                Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 cridegelaladardarderiedagakreicelaladakenderenterentakerekeeneera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 GGCCTCGACCTCGACGAAGCCCTCGCCGCAGGTCTGCGCCCCCGGCGTCACCCCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 AAAGGCGACCGCGACGGCGGGTTCACCGTC----CTCGGCAACTACATCGGCGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 GOCAACCCGCAGACACCAAGCCAGAGAAGATCGACATGACCGCGCCGGTCATCACCTCC
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Hou Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ry Match 13.2%; Score 56.2; DB 7; Length 2640; t Local Similarity 51.1%; Pred. No. 0.31; ches 161; Conservative 0; Mismatches 148; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2640 BP; 602 A; 717 C; 823 G; 498 T; 0 U; 0 Other;
   SA,
Zhu
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   Goff
   Glazebrook J, G
Whitham S, Xie
                                                                                                                                                                                                                                                                                                                                                                   Claim 6; SEQ ID NO 3257; 899pp; English
Cooper B,
S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC08080 standard; DNA; 2640
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                                                                                                              WPI; 2003-175290/17.
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                                                                                                                                                                                          complement (4. .1824)
                                                                                                                                                                         Location/Qualifiers
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56829. .58019
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complement(58756.
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complement(61798.
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                                                                                                                                                                                                                                         gene
                                                                                                                                         Streptomyces nodosus
                                             26-JUN-2003
               AAD54645
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This invention, in the area of plant biotechnology, relates to novel polynucleotides comprising a nucleotide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or which is up-regulated with the synthesis, metabolism or which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco, sugarbeet, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is a DNA sequence encoding a rice protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                  New plant genes encoding polypeptides having an activity involved in or
associated with the synthesis, metabolism or degradation of carbohydrates
in the plant grain useful in generating plants having improved
nutritional properties.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 GGCCTCGACCTCGACGAAGCCCTCGCCGCAGGTCTGCGCCCCGGCGTCACCCCGCCA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 GGCAACCCGCAGAACACCCAGAGCCAGAGATCGACATGACCGCCGCCGGTCATCACCTCC 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 GGCGAGCCCGAGAGTATCGCCATGACGGCCCGGTCATCACCTCCGGTGAGCCTGAGCCG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 CTGGGCAAGATCACGGTGGAGACGCCAAGCACGAGGTGCTCCACACCGGCGGCGGCTAC 72
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Ricke D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2640 BP; 602 A; 717 C; 823 G; 498 T; 0 U; 0 Other;
                                                                                                                                                                       Cooper B, Goff SA,
Kreps J, Provart N,
                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 347; 130pp; English
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ID AAD54645 standard; DNA; 113193
                                                                        22-JUN-2001; 2001US-0300112P.
26-SEP-2001; 2001US-0325277P.
20-DEC-2001; 2001US-0342327P.
                                           21-JUN-2002; 2002WO-IB002450.
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Glazebrook J, Katagiri F,
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P-PSDB; ADC08081
             03-JAN-2003
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S. nodosus
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product= "Cytochrome P450 encoded by S. nodosus amphi
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/*tag= f
Product = "Polyketide synthase multienzyme housing
extension modules 18 and thioesterase encoded by S.
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Streptomyces nodosus amphotericin (amph) biosynthetic gene cluster
                                 Polyene; antibiotic; amphotericin; amph; polyketide; enzyme; gene;
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product= "Polyketide synthase multienzyme housing
loading module encoded by S. nodosus amph gene"
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/product= "GDP-mannose dehydratase encoded by
amphDIII gene"
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(pos:59869. .59871, aa:Met)
.61995)
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'rtag= n
'product= "Glycosyl transferase encoded
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/product= "Ferredoxin encoded by S.
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/product= "ABC transporter encoded
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/transl_except= (pos:65773.
66081. 70319
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Mon Aug

(NOVO ) NOVO NORDISK BIOTECH INC. (NOVO ) NOVO NORDISK AS. WPI; 2000-594572/56. 40200056762-A2 22-MAR-1999; 13-MAR-2001 28-SEP-2000. Berka RM, 305 AAF12486; 365 28092 28032 RESULT 14 AAF12486 D ò g ò The invention relates to the gene cluster encoding the polypeptides responsible for the biosynthesis of the polyene antibiotic amphotericin (amph) of Streptomyces nodosus. Polywucleotides of the invention are useful for preparing amphotericin derivatives or analogue antibiotic agents with altered properties and in the biosynthesis of polyketides other than amphotericin. ampholii, ampholi or ampholi mutants are useful of for producing amphotericin derivatives glycosylated with alternative sugars, amphotericin ampholii gene sequences are useful in engineered biosynthesis of perosaminyl-amphoteronolide B; ampholii and perosaminyl-i6-descarboxyl-16-methyl amphoteronolide B; ampholii and ampholi gene sequences are useful for preparing polymethesis of perosaminyl-i6-descarboxyl-16-methyl amphoteronolide B; ampholii and ampholi gene sequences are useful for preparing polymetides capable of addition of mycosamine to a polyketide other than amphoteronolide A or B or for preparing polymetides for in vitro synthesis of GDP-mycosamine. The present sequence is S. nodosus amph biosynthetic gene cluster 27911 27912 AACTCGGCCGGCTCGGCGCCGAGGTCACGTCGCCCCGTACGACGGCGGCGACGGGAACG 27971 27851 o, 244 124 184 64 65 GCGCCGGACTGACCAAGAGCGAGTTGGCCAGGCGCATCCAGAAGGACCGGGCCACCGTCG 27852 gecregraciaeciaecrececeseceaeaeareceaeceaeaeaeaeaeaeaeaeeee 125 GCCGCTGGGAGGACGGCAAGAACCGGCCCGACGACGCGGGACCTCGTTGCCCCGCGTCGCCC Novel cytochrome P450 enzyme and nucleotides encoding the enzyme, use: for preparing amphotericin derivative or analog antibiotic agent with altered properties, in biosynthesis of polyketide other than Sequence 113193 BP; 14248 A; 45141 C; 38354 G; 15450 T; 0 U; 0 Other; P-PSDB; AAE36116, AAE36117, AAE36118, AAE36119, AAE36120, AAE36121, AAE36122, AAE36123, AAE36124, AAE36125, AAE36126, AAE36127, AAE36128, AAE36129, AAE36130, AAE36131, AAE36132. Gaps /product= "Polyketide synthase multienzyme housing extension modules 1 and 2 encoded by S. nodosus by /product= "Polyketide synthase multienzyme housing extension modules 3, 4, 5, 6, 7 and 8 encoded by S. . 0 Length 113193;

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28091
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245 CCCCGCCAGCGACCCCAACCATGGACCTGGACGAAATCGAGCTGGTCCGCACCGACC 304
                                                              ceaceacrecreakeacaracarecrerreacreceacacaeacaraaaacarec
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Aspergillus oryzae EST SEQ ID NO:5009. AAF12486 standard; cDNA; 662 BP. (first entry)

Multiple gene expression, filamentous fungal cell, EST, expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryvae; Trichoderma reses; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.

Aspergillus oryzae.

22-MAR-2000; 2000WO-US007781.

99US-00273623

Olsen PB; Clausen IG, Rey MW, Shuster JR, Kauppinen S, Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags.

Claim 88; Page 2105; 3161pp; English.

The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the responsion of the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the came genes in one or more second filamentous fungal cells. Monitoring the companions to be improved. New genes may be discovered, the microorganisms to be improved. New genes may be discovered, or possible functions of unknown open reading frames can be identified and genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, advantages over genomic or random CDNA clones including element.

CC genes capabolic pathway engineering. Using ESTS provides several advantages over genomic or random CDNA clones including element.

CC and organisation of the microarrays based on function of the gene and organisation of the microarrays based on function of the ESTS from Fusarium venenatum; AAF11248 to AAF11877 represents ESTS from ESTS from Fashibs4 to AAF11878 represents

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66546. .67370
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70099. 70662
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'product= "Protein of ORF 13"
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9713. 65800
*tar-
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87372. .86803
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32587. .84446
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15880. .19035
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                                                                                                                                                                                                                                      GAAGGACCGGGCCACCGTCGGCCGGTGGGAGGACGGCAAGAACCGGCCCGGACGACGCGGA
Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ramoplanin; ramoplanin biosynthetic pathway polypeptide; antibiotic; biosynthesis gene cluster; bioengineering; peptide synthetase module; adenylation domain; hydroxyphanylglycine; HPG; antibiotic precursor; chlorinate; lipdepsipeptide; gene; ds.
                                                                                                                                    Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88421nt genomic DNA of ramoplanin producing Actinoplanes sp.
                                                                                                Score 56; DB 3; Length 662;
Pred. No. 0.39;
0; Mismatches 125; Indels
                                                                  Sequence 662 BP; 127 A; 257 C; 143 G; 133 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "cay="Protein of ORF 1"
product= "Protein of ORF 1"
*tag= b
product= "Protein of ORF 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /4038. .5048
/*tag= c
/product= "Protein of ORF 3"
complement (6665. .5814)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "Protein of ORF 4"
complement(7703. .6693)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= e
/product= "Protein of ORF 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9691. .10761
/*tag= g
/product= "Protein of ORF 7"
complement(12751. .10829)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= h
/product= "Protein of ORF 8"
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product= "Protein of ORF 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (9464. .8130)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
2077. .3078
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAL40781 standard; DNA; 88421 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                          CGAGCTGGTCCGCACC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 CGGCAAGAACGGCACC 426
                                                                                                  13.1%;
51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                  Best Local Similarity 51.2
Matches 131; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-OCT-2002
                                   invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAL40781;
                                                                                                                                                                                                                                      105
                                                                                                                                                                                                                                                                                                      165
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                                                                                                   Query Match
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P-PSDB; AGC2146, AAO22147, AAC22148, AAO22149, AAO22150, AAO22151, AAO22152, AAO22153, AAO22153, AAO22153, AAO22154, AAO22155, AAO22156, AAO22157, AAO22158, AAO22165, AAO22165, AAO22165, AAO22165, AAO22165, AAO22165, AAO22167, AAO22167, AAO22167, AAO22172, AAO22177, AAO22177,
/*tag= ag
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                                                                                                                                                                                                                                                                                                                                                                                           (ECOP-) ECOPIA BIOSCIENCES INC.
                                                                                                                                                                                                                                                                    13-OCT-2000; 2000US-0239924P.
12-APR-2001; 2001US-0283296P.
24-JUL-2001; 2001US-00910813.
                                                                                                                                                                                                          15-OCT-2001; 2001WO-CA001462
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zazopoulos E,
                                                                                      WO200231155-A2
                                                                                                                                                .8-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Farnet CM,
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The invention relates to an isolated ramoplanin biosynthetic pathway polypeptide selected from a polypeptide of open reading frames (ORF) 1-32. The isolated polypeptide are useful for chemically modifying a biological molecule that is a substrate for a polypeptide encoded by a campolanin biosynthesis gene cluster, by contacting the biological contacting the biological molecule. The method comprises contacting the biological molecule with the lasolated polypeptide, where the polypeptide chemically modifies the biological molecule. The method comprises contacting the biological molecule with at least two different polypeptides concoded by ramoplanin ORFS 1-31. The polypeptides are useful for directing the biological molecule with a least two different polypeptides encoded by ramoplanin ORFS 1-31. The polypeptides are useful for directing the biosopratical generating of antibiotic structures. An isolated polypeptide or its concoding mucleic acid sequence is useful for generating derivatives of ramoplanin for improving production or for producing variants of other antibiotics of the peptide class. The isolated polypeptides are useful for sequence in conjunction with other peptide antibiotic precursor, for modifying the containing peptide antibiotic, for minating farty acid structure and/or enhancing farty acid incorporation of the very peptide antibiotic structure, for production of an hydroxyphenylglycine (HPG)-containing peptide antibiotic, for enhancing secretion of ramoplanin products or its variants or derivatives, to chlorinate HPG of remoplanin products or its variants or derivatives, to chlorinate HPG of remoplanin products or its variants or derivatives, to chlorinate HPG of peptide antibiotic precursor, and for designing specific nucleotide generative producing microorganisms. This polymolectide sequence represents the containing the peptide antibiotic producing microorganisms. This polymolecule sequence represents the containing products or a moptimic products or a remoplanin products or a geptide sequen Novel isolated ramoplanin biosynthetic pathway polypeptide useful for chemically modifying biological molecule that is a substrate for a polypeptide encoded by a ramoplanin biosynthesis gene cluster. Sequence 88421 BP; 10639 A; 32391 C; 32663 G; 12728 T; 0 U; 0 Other; Disclosure, Page 87-135; 212pp; English,

27 cesca catesesce catacetecte cece ceces eseces ces ces cates con a contrate con a contrate con a contrate con Query Match
Best Local Similarity 51.9%; Pred. No. 0.3;
Matches 153; Conservative 0; Mismatches 136; Indels 6:

39811 CGGCACGTCGACGCCGCCGCCCTCGAAACCGCCCTGCGCGACGTGCTGGAGCGGCACGA 39870

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39925 eccecrceacidae accedentica eccuada en caracidade a con caracidade a con contra con contra con contra 147 CCGGCCCGACGACGCGGACCTCGTTGCCCGCGTCGCCCAGGTGCTCGGCCTCGACCTCGA 206 207 CGAAGCCCTCGCCGCCGCAGGTCTGCGCCCCCGGCGTCACCCCCCCAGCGACCCCAACCAT 267 GGACCTGGACGAGAAATCGAGCTGGTCCGCACCGACCCCAAGCTGGACGAGGAC 321 g ò В ò

6, 2004, 09:47:31 Search completed: August Job time: 256.157 secs

Staffa A;

Sequence 5192, Ap Sequence 6283, Ap Sequence 3820, Ap Sequence 3691, Ap Sequence 376, Ap Sequence 5965, Ap Sequence 5965, Ap Sequence 5922, Ap Sequence 6329, Ap Sequence 6329, Ap Sequence 6420, Ap

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCATCATCGCCCTAATCCTGGAGCGCCGTGAGCGCGCGACAGCGGCGATCGAGGA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          683 CCGGCCGCGCCTCGCGGACCGGTGCGAGATCCTGCCCGGCGACTTCTTCGAGACCATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1

US-09-266-965-66

Sequence 66, Application US/09266965

Ratent No. 6495348

GENERAL INFORMATION:
APPLICANT: Sherman, D
APPLICANT: Sherman, D
APPLICANT: Waroglu, M
APPLICANT: He, M
APP
US-09-252-991A-5192
US-09-252-991A-5183
US-09-252-991A-3696
US-09-252-991A-3691
US-09-252-991A-3776
US-09-252-991A-3776
US-09-252-991A-5908
US-09-252-991A-5908
US-09-252-991A-5908
US-09-252-991A-6918
US-09-252-991A-6826
US-09-252-991A-6918
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Sequence 551, Appl
Sequence 5609, Ap
Sequence 5609, Ap
Sequence 3697, Ap
Sequence 3697, Ap
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 74, Appl
Sequence 94, Appl
Sequence 945, Ap
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                                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-09-252-991A-313
US-09-103-840A-1
US-09-252-991A-313
US-09-252-991A-313
US-09-103-840A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          682709 segs, 277475446 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                           nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0 ... Maximum DB seq length: 2000000000
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426
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US-09-252-991A-5600/c
; Sequence 5600, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
                                   TYPE: DNA
CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-5631
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Best Local Similarity 49.1%;
Matches 173; Conservative
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LENGTH: 1299
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF ILVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PELLE REPERENCE: 107196.136
CURRENT PELLING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILLING DATE: 1998-02-18
PRIOR PILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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923 TCGTCCTCGTCGGCGCCGCGAACGCTCGGAGAGCGAATTCGCCGCGCGCTGCTGGAGAA 980
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APPLICANT: Mao, Y
APPLICANT: Mao, Y
APPLICANT: Mao, Y
APPLICANT: Warglu, M
APPLICANT: Sheldon, P
TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
FILE REPERENCE: 600.456US1
CURRENT PILING DATE: 1999-03-12
CURRENT PILING DATE: 1999-03-12
CURRENT PILING DATE: 1996-08-19
EARLIER APPLICATION NUMBER: US 08/624,447
EARLIER PILING DATE: 1994-00-06
EARLIER FILING DATE: 1994-10-06
EARLIER FILING DATE: 1994-10-07
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Pred. No. 0.00016;
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                                                                                                                                                                                                     ; Sequence 76, Application US/09266965; Patent No. 6495348; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
, ORGANISM: Streptomyces lavendulae
US-09-266-965-76
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Best Local Similarity 51.0%;
Matches 152; Conservative
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US-09-252-991A-5631
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APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEEC ACID AND THERAPEUTICS
FILE REFERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRICR FILING DATE: 1999-02-18
PRICR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 5600
LENGTH: 1611
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                                                               Gaps
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Score 54.4; DB 4; Length 1
Pred. No. 0.013;
0; Mismatches 176; Indels
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FALCENT NO. 6591/95
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
ARC J. ARC J. AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION:
ARC J. ARC J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 52; DB 4; Length 939;
Pred. No. 0.039;
0; Mismatches 210; Indels
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Pred. No. 0.039;
0; Mismatches 210; Indels
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788,
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3645
LENGTH: 939
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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US-09-252-991A-3697
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ilarity 47.3%;
Conservative
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Best Local Similarity 47.3%;
Matches 194; Conservative
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US-09-252-991A-3697
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LENGTH: 1881
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Best Local 8
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Sequence 5665, Application US/09252991A

Patent No. 6521795

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

FILE REFRENCE:

FILE REFRENCE:

FILE REPRENCE:

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Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
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        1039 CGCCGTGCAGGTGGAAACCACCGCGCGCGCGGGTCGGCGCGTGATCAGCATGCC 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 CGGCCGGTGGGAGGACGGCAAAACCGGCCCGACGACGACGACGTCGTTGCCCGCGTCGC 182
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                                                                                                                                      CCCCAAGCTGGACGACGACATGAAGCGGCGCATCATCGCCCTAATCCTGGAGCGCCGTGA 362
                                                                                                                                                                                                                       cenaracerceacercercececececececentearceacercarceacercarcaece 920
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                                                                                                                                                                                                                                                                                                                 363 GCGCGACAAGGCGGCGATCGAGGAAACCAAGCGGCTCATCGACCTGTTC
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Pred. No. 0.013;
0; Mismatches 176;
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Best Local Similarity 49.1
Matches 173; Conservative
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US-09-252-991A-5605
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                             314 ACGAGGACATGAAGCGGCGCATCATCGCCCTAATCCTGGAGCGCCGTGAGCGCGACAAGG 373
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12.0%; Score 51; DB 2; Length 44377;
Best Local Similarity 47.9%; Pred. No. 0.065;
Matches 147; Conservative 0; Mismatches 160; Indels
                                                                                                                                                                                                                                                                                                      374 CGGCGGCGATCGAGGAAACCAAGCGGCTCATCGACCTGTTCCGCCGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7. Application US/08804227C
| Patent No. 5876991
| GENERAL INFORMATION:
| APPLICANT: DeHOff, Bradley S. |
| APPLICANT: Kuhstoss, Stuart A. |
| APPLICANT: Rosteck, Paul R. J. |
| APPLICANT: Sutton, Kimberly L. |
| TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES |
| NUMBER OF SEQUENCES: 15 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: THOMAS G. PLANT 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : LILLY CORPORATE CENTER INDIANAPOLIS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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IBM Compatible
SYSTEM: MS-DOS
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
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CITY: IN
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3812
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419 CGCTGCCCGGACGCGCCGTGCTGGACGCCTACGTCGGCGACATCGACCGTTTCGTCGGCA 478
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Pred. No. 0.039;
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Sequence 3812, Application US/09252991A
Patent No. 655/795
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
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Matches 194; Conservative
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                                                                                                                                                                                                                                                                   Length 44377;
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APPLICANT: Sherman, D

APPLICANT: He, M

APPLICANT: Sheldon, P

TITLE OF INVENTION: MICOMYCIN biosynthetic gene cluster

FILE REFERENCE: 600.456031

CURRENT APPLICATION NUMBER: US/09/266,965

CURRENT FILING DATE: 1996-08-19

EARLIER PILING DATE: 1996-08-19

EARLIER FILING DATE: 1994-10-06

EARLIER FILING DATE: 1994-10-06

EARLIER FILING DATE: 1994-10-06

EARLIER FILING DATE: 1993-10-07

SERVING SEQ ID NOS: 145

SOFTWARE: FESTSEQ for Windows Version 3.0

SEQ ID NO 2.2

TENDERH: 1720
                                                                                                                                                                                                                                                                                                                                       0; Mismatches 160; Indels
                                                                                                                                                                                                                                                               Score 51; DB 2;
Pred. No. 0.065;
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Best Local Similarity 47.5%;
Matches 150; Conservative C
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Best Local Similarity 47.99
Matches 147; Conservative
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31329..36071
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NAME/KEY:
LOCATION:
FEATURE:
                                                                                                           ; NAME/KEY:
; LOCATION:
US-08-804-198-1
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                                       74 TGACCAAGAGCGAGCCAGGCGCATCCAGAAGGACCGGGCCACCGTCGGCCGGTGGG 133
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APPLICANT: Burgett, Stanley G.
APPLICANT: Rubstoss, Stuart A.
APPLICANT: Rubstoss, Stuart A.
APPLICANT: Robert, Nark A.
APPLICANT: Rochardson, Mark A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: USA
ZIP.
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Macintosh

COMPUTER: Microsoft Word 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/804,198

FILING DATE:
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ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REFERENCE/DOCKET NUMBER: 36,470
REFERENCE/DOCKET NUMBER: 99113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 31,-276-3885
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
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20110..31284
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MOLECULE TYPE:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                 1101 CGGCCTCGTCACGCGCTTCCCCGGCCTGCGCATGGCCGCCGCGCCCGAGGACATCCGCTG 1160
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GAAGACCGGGGAGTCCCTGCTGGCCTGCCGCCGCCCACCCGCGGACCCCGCCGTCTT 980
                                                                             CGCCGCAGGTCTGCGCCCCGGCGTCACCCCGCCAGCGACCCCAACCATGGACCTGGACGA 278
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Pred. No. 0.083;
0; Mismatches 166; Indels 0;
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APPLICANT: Waroglu, M
APPLICANT: He, M
APPLICANT: Sheldon, P
TITLE OF INVENTION: Micomycin biosynthetic gene cluster
FILE REFERENCE: 600.456US1
CURRENT PILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: US 08/624,447
EARLIER APPLICATION NUMBER: PCT/US94/11279
EARLIER FILING DATE: 1994-01-0.
EARLIER PLING DATE: 1994-10-06
EARLIER RILING DATE: 1994-10-06
EARLIER APPLICATION NUMBER: US 08/133,963
EARLIER FILING DATE: 1994-10-06
EARLIER APPLICATION NUMBER: 145
NUMBER OF SEQ ID NOS: 145
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-266-965-74
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Best Local Similarity 47.5%;
Matches 150; Conservative
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GENERAL INFORMATION:
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US-09-266-965-74
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US-05-252-991A-9345/c

1 Sequence 9345, Application US/09252991A

2 Sequence 9345, Application US/09252991A

3 Sequence 9345, Application US/09252991A

3 FILE NEW MAC J. Rubenfield et al.

APPLICANT: MAC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US/06/4,788
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0; Mismatches 166;
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1989-02-18
1981: US 60/074,788
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; ORGANISM: Streptomyces lavendulae
US-09-266-965-96
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Matches 150; Conservative
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Search completed: August 6, 2004, 13:42:31
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US-09-252-991A-9429
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US-09-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-252-991A-9-
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                                                                                                                                                                                                                                                                                                                                                                                Score 50.2; DB 4; Length 1 Pred. No. 0.087; 0; Mismatches 193; Indels
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9345
LENGTH: 1344
                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-9429
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Best Local Similarity 47:7%;
Matches 179; Conservative
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104 AGAAGGACCGGCCACCGTCGGCCGGTGGGACGGACGGCAAGAACCGGCCCGACGACGCGG
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		AL066051 Drosophil	AL053013 Drosophil	AL108460 Drosophil	BE401996 CSB003D02
COLUMNIC			ID		CNS006XK	CNS0091P	CNS017SY	BE401996
			DB	1	C) O)	5	20	10
			Match Length DB		935	925	1101	582
	40	Query	Match		8 16.4	14.8	14.7	14.6
			Score		69.8	63	62.8	62.4
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3 BRY_32	5 wpalc.	4 MUG020	1 WHE416	6 AZ02.1	4 AZ02.1	9 MUG002	0	9 HX01PC	9 WHE322	S AWBO11.	0 HZ51F0	3 Drosop	9 WHE096	9	3 OV.001	0 WHE047	3 CSB002	2 BRY 33	7 wiplc.pk	6 PSR6635	Н	Ŋ	σ	Н	7	0	ო	<b>,</b> −1	0	ß	9	9	æ	S	50624	18083	m	99317	1729	52002	
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## ALIGNMENTS

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Drosophila melanogaster genome survey sequence TET3 end of BAC #BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 BVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns EAC-fr
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
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Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BcoxI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                 /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db xref="taxon:7227"
/clone="BRTA14N09"
/clone lib="RRCI-98"
/note="end : T7"
                                                                                                                                                                                                                                                                                                                                                        16 4%; Score ...
30.8%; Pred. No. 1.8;
-ive 93; Mismatches 168;
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melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC ilbrary was prepared by Karutoyo Ossegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
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ALI08460. ALI08460.
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Submitted (23-UUL-1999) Genoscope - Centre National de Sequencage :
Submitted (23-UUL-1999) Genoscope - Centre National de Sequencage :
Br 191 911006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of
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Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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BDGP is constructing a physical map of the Drosophila
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                                                                                                                                                                                                                                                                                                                             /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
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/clone="BACR19D16"
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/mol_type="mRNA"
/cultivar="Wyuna"
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Enkaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Eureptophyta; Doales; Poaceae;
Pooideae; Triticeae; Triticum.
Entaryota; Doales; Triticum.
Entaryota; Doales; Triticum.
Entares 1. (Bases 1.0. 582)
S. Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T.,
Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A.,
Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J.,
Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P.,
Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G.,
Shariflou, M., Sorrells, M., Warbuton, and Wenzel, G.
International Triticeae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
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CSB003D02F990908 ITEC CSB Wheat Endosperm Library Triticum aestivum
EDNA clone CSB003D02, mRNA sequence.
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collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melangaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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RNA linear EST 25-JUN-2002 Triticum aestivum cDNA 5',
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/clone="CSB003D02"
/clone="CSB003D02"
/clone="CSB003D02"
/dev stage="endosperm"
/lab_host="Escherichia coli SOLR"
/clone lib="ITEC CSB Wheat Endosperm Library"
/note="Vector: Lambda Zap/Bluescript; Site 1: XhoI;
Site 2: EccRI; Plants grown in Phytotron with 18C/13C
(day/night) 16 hour light. M13 Reverse sequencing primer used. 1.0 Kbp average insert size."
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1; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 GCCGGACTGACCAAGAGCGAGTTGGCCGAGGCGCATCCAGAAGG----ACCGGGCCACCGTC
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1 (bases, Leambrecht, M. and Rhee, S.Y.
Arabidopsis genomic information for interpreting wheat
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Contact: Appels R
Div. of Plant Industry, CSIRO
Div. of Plant Industry, CSIRO
Tel: 61 62 465496
Fax: 61 62 465000
Fax: 61 62 465000
International Triticeae EST Cooperative (ITEC)
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Funct. Integr. Genomics 3 (1-2), 33-38 (2003)
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50.9%; Pred. No. 19;
tive 0; Mismatches 166;
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BRY 3207 wheat EST endosperm library
mRNA sequence.
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Location/Qualifiers
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Triticum aestivum
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Sp4 bp mRNA linear EST 21-NOV-2002

Wpalc.pk016.nlO wpalc Triticum aestivum cDNA clone wpalc.pk016.nl0

Sp8.end, mRNA sequence.
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Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation May, P.O. Box 6104, Newark, DE 19714-6104, USA
                                                                       Contact: Lambrecht M
The Arabidopsis Information Resource
Carnegie Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
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/dev_stage="developing endosperm tissue
(days_post_anthesis]"
/clone_lib="wheat_EST_endosperm_library"
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Pred. No. 19;
0; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Triticum aestivum (bread wheat)
Triticum aestivum
                                                                                                                                                                                                                                                                                                                                            Email: rhee@acoma.stanford.edu.
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/cultivar="Wyuna"
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Triticum aestivum (bread wheat)

Triticum aestivum

Triticum aestivum

Eukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticaee; Triticum.

E 1 (bases 1 to 620)

Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T.,
Cloutier,S., Dubcovsky,J., Fewiller,C., Gale,W., Graner,A.,
Gustafson,P., Laroy, Hermann,R.G., Holton,T., Jacquemin,J.M., Jia,J.,
Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P.,
Oginara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G.,
Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.,
International Triticeae EST Cooperative (ITEO): Production of
Expressed Sequence Tags for Species of the Triticeae
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MGG020.D01R990620 ITEC MUG Wheat Spikelet Library Triticum aestivum
EB417374
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Tel: 81 45 820 1903
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                                                                                                                                                                                                                /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCGGACTGACCAAGAGCGAGTTGGCCAGGCGCATJCCAGAAGG---ACCGGGCCACCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 14; Length 594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 CGCGACAAGGCGGCGGCGATCGAGGAAACCAAGCGGCTCATCGA 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 62.4; DB 14;
Pred. No. 19;
0; Mismatches 166;
                                                                                                                                                         1. .594
/organism="Triticum aestivum"
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seg primer: M13.
                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE417374.1 GI:9415220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.6%;
50.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity 50.9
175; Conservative
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source

FEATURES

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/db.xref="taxon:4565"
/clone="WHE4463 C06_E11"
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/tissue_Type="Roots, leaves, crown, stem and sheath"
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/clone lib="Wheat CS Whole plant cDNA library"
/clone lib="Wheat CS whole plant cDNA library"
/clone lib="Wheat CS whole plant cDNA library"
/note="Yector: Lambda Uni-ZAP KR, excised phagemid
pBluescript SK(-); Site_1: EcoRI; Site_2: KhoI; Plant
tissues from wheat cv. CS grown to full tillering stage in
greenhouse were collected at University of California,
Davis (Jan Dvorak's lab, K. Deal and E. Akhunov). Total
RNA was prepared from leaves (young leaf and third leaf),
whole roots, crown, steam and sheath tissues, and then
equal quantities of RNA were pooled from the these
samples. PolyA was purified from the pooled from the these
to give pBluescript SK(-) phagemids in J. Dvorak's lab (to give pBluescript SK(-) phagemids in J. Dvorak's lab (to give pBluescript SK(-) phagemids in J. Dvorak's lab (suppression) y Dvorak at the University of California,
Davis. Colony plating, plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      690 bp mRNA linear EST 11-JUL-2003
Triticum aestivum cDNA clone AZO2112G03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCCGCCAGCGACCCCAACCATGGACCTGGACGAGAAATCGAGCTGGTCCGCACCGAC 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cechaceaccaeadecriceschaderecricecesedercaccaricececaegesere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gecegagagagagagagecegrgaccegrccaccaagecegecrccagrrccegrc
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                                Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: SX primer: SX primer. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    crecceaacarcaccegrecrecreceaagaccrecida 408
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Pred. No. 19;
0; Mismatches 166;
                                                                                                                                                                                                                                  organism="Triticum aestivum"
                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/cultivar="Chinese Spring"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triticum aestivum (bread wheat)
Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD869706
AZO2.112G03F001120 AZO2
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SOURCE
ORGANISM
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DEFINITION
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CD869706
                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
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Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
                                                                                                                                                                                                                                                                      /mol type="mmm."
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Xhol; MI3 Reverse sequencing primer used. 1.2 Kbp average
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Triticum
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s; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyte Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticaa; Triticum.

| Pooideae; Triticaa; Triticum.
| (basea: 1 to 673)
| Anderson,O.D., Akhunov,E., Chao,S., Crossman,C., Deal,K., Dyorak,J., Lazo,G.R., Rausch,C.J., Wilson,C. and Woo,J.
| Hostructure and function of the expressed portion of the wheat genomes - Chinese Spring whole plant cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCAAGCTGGACGACATGAAGCGGCGCATCATCGCCCTAATCCTGGAGCGCCGTGAG
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Fax: 81 45 820 1901

Email: ogihara@yokohama-cu.ac.jp
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
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14.6%; Score 62.4; DB 10;
Best Local Similarity 50.9%; Pred. No. 19;
Matches 175; Conservative 0; Mismatches 166;
                                                                                                                                                                                                                                          organism="Triticum aestivum"
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Triticum aestivum
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AZO2.101A18F010111 AZO2 Triticum aestivum cDNA clone AZO2101A18,
mRNA sequence.
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Popernatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
(bases 1 to 694)
                                                                                                                                                 This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr)
                                           Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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                                                                                                                                                                                                                                          /mol_type="mRNA"
/cultivar="recital"
/db_xref="taxon:4565"
/clone="AZO2112G03"
/tissue_type="root"
/clone_lib="AZO2"
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Triticum aestivum
Pooideae; Triticeae; Triticum.
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Triticum aestivum (bread wheat)

Triticum aestivum

Eukaryota; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Triticum.

E 1 (bases 1 to 872)

S Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T.,

Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A.,

Gustafson, P., Largridge, P., Lazo, G.R., Lin, J.J.,

Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J.,

Oginara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G.,

Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G.,

International Triticeae BST Cooperative (ITEC): Production of

Expressed Sequence Tags for Species of the Triticeae
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Kihara Institute for Biological Research, Yokohama City University
Maloka-cho 641-12, Totsuka-ku, Yokohama 244-0813, JAPAN
Tel: 81 45 820 1903
Fax: 81 45 820 1901
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Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infoblogen.fr).
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Pred. No. 19;
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Mon Aug 9 10:16:09 2004
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/clone_lib="TEC MUG Wheat Spikelet Library"
/note="Vector: pBluescript Sk(-); Site_1: EcoR1; Site_2:
Xhol; M13 Reverse sequencing primer used. 1.2 Kbp average
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1 (bases 1 to 1035)
Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D., Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A., Links,M.G., McCarthy,E.L., Monroy,A., Murak,I., Nilson,D., Penniket,C., Roach,J.L. and Sarhan,F.
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University of Saskatchewan, Department of Computer Science
ICO1 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N SA9, Canada
Tel: 306 966 1769
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Email: ogihara@yokohama-cu.ac.jp
International Tritticeae EST Cooperative (ITEC)
http://what.pw.usda.gov/genome.
Location/Qualifiers
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Library (
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                                                                                                                                                                                                                                                   organism="Triticum aestivum"
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FGAS024469 Triticum aestivum FGAS:
aestivum cDNA, mRNA sequence.
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Contact: Wm L Crosby
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Best Local Similarity 50.9%
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/clone libe "Titulcum adescivum FGAS: Library & CAF Cown (50%) and leaf (50%) tissues from wheat cultivar Norstar after short exposure times to low temperature in the light and in the dark. L2 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 2005 from wheat cultivar Norstar after short exposure times to low temperature in the light and in the dark. L2 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 200, wheat plants were transferred to 4C in the light. Lam crown sections and green leaf tissu were separately harvested after 1, 3, and 6 hours of low temperature exposure. The last 6 populations: After 7 days of growth at 20C, wheat plants were transferred to 4C in the dark. Lam crown sections and green leaf tissu were separately harvested after 1, 3, and 6 hours of low temperature exposure. First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI. In addition, this library used a primer for second strand synthesis that annealed to an artificial sequence (RNA oligo) added before first strand synthesis. Therefore when sequences from EST generated from this library will be masking step will have to be included to mask this RNA masked for vector and adaptor sequences, an additional masking step will have to be included to mask this RNA masked for vector and adaptor sequences, an additional
Email: fgas_ests@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [21,782].
Plate: L68006 row: E column: 04.
Location/Qualifiers
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/organismENA"
/mol_type="mENA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 6_CAP GATE 1"
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/note="Vector: pBluescript SK+; Site_l: EcoRI (5'-end of CDNA); Site_2: XhoI (3'-end of CDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, Sali,PStI). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable."
        BQ470159 599 bp mRNA linear EST 30-MAY-2002
MXO1804T HX Hordeum vulgare subsp. vulgare cDNA clone HX01P04
5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                               Hordeum vilgare subsp. vilgare
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Poaceae;
Pooideae, Triticaee, Hordeum.

1 (bases 1 to 599)

Lang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.

EST sequencing and analysis in barley (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      325 récrédecardégaaceaceagaderéggagérédrégégégégégéréaceardegée 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
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Pred. No. 20;
0; Mismatches 183; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: stein@ipk-gatersleben.de
Insert Length: 599 Std Error: 0.00
Plate: 1 row: P column: 4
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/cultivar="barke"
/sub_species="vulgare"
                                                                                                                                                                                                                                       Hordeum vulgare subsp. vulgare
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                                                                                                                                                          BQ470159.1 GI:21277941
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Best Local Similarity 48.5%;
Matches 172; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Stein Nils
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| organism="Triticum aestivum"
| mol_type="mixid"
| well_type="mixid"
| cultivar="Chinese Spring" |
| clole="WHEN5215_Clo_E19" |
| clone="WHEN525_Clo_E19" |
| tissue_type="Anther" |
| dev_stage="Melotic stages pre-meiosis-metaphase I" |
| lab_host="E. coli DHIOB" |
| clone lib="Wheat melotic anther cDNA library" |
| clone lib="Wheat melotic anther cDNA library" |
| clone lib="Wheat melotic anther cDNA library" |
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| clone lib="Wheat melotic anther cDNA library |
| clone lib="Wheat melotic anther stage was determined by removing anthers from individual primary florets. One anther was sacrificed for microscopic staging, and if determined to be between (and including) melotic stages pre-melosis and metaphase I, the remaining two anthers were collected and pooled for library construction. The tissue, total RNA, and poly(A) RNA were prepared, cDNA synthesised, and directionally ligated into pSPORTI by Tim Sutton in the P Langridge Lab at the Department of Plant Science, University of Adelaide, Waite Campus, Australia. Average insert size 1.5Kb. Plasmid DNA Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                               CA497279
WHE3225_CIO_E192T Wheat meiotic anther cDNA library Triticum aestivum cDNA clone WHE3225_CIO_E19, mRNA sequence.
CA497279
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US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: $10559573
Fax: $105595818
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Triticum aestivum
Triticum aestivum
Bukaryora, Viridiplantael, Streptophyta; Embryophyta; Tracheophyta;
Bukaryora, Viridiplantael, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticum.
Tri
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385 ACGCGGCGTGCTCCCAACATCAACCCCGTGCTGCTCCCCAAGAAGGCCCTCGA 439
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Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: 17 primer.
Location/Qualifiers
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50.3%; Pred. No. 21;
ive 0; Mismatches 150; Indels
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us-09-855-340a-2.rst

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124 GGCCGGTGGGAGGACGGCAAGAACCGGCCCGACGCGGACCTCGTTGCCCGGTCGCC
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Job time :
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Triticum aestivum (bread wheat)

Entaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

E (bases 1 to 424)

S Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloulier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Langridge, P., Laco, G.R., Lin, J.J., McGuire, P., Langridge, P., Laco, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Werzel, G.

International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev stage="meiotic stage no later than metaphase I" /clone lib="ITCC ANB Wheat Meiotic Stage Library" /note="Wector: pSport I (Life Technologies cat. no. 18248-013); Site 1: Sall; Library constructed in pSport 1. Directionally cloned using the Superscript Plasmid System for cDNA synthesis and plasmid cloning. M13 Reverse sequencing primer used to obtain 5' sequence data. 1.4 Kbp average insert size."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Langridge P
Special Research Centre, Basic and Applied Plant Molecular Biology
Waite Campus, University of Adelaide, Glen Osmond SA 5064 AUSTRALIA
TT=1: 61 8 8303 7368
Fax: 61 8 8303 7102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE400165
AWB011.D10F000328 ITEC AWB Wheat Meiotic Stage Library Triticum aestivum cDNA clone AWB011.D10, mRNA sequence.
BE400165
    CATGGACCTGGACGAGGAAATCGAGCTGGTCCGCACCGACCCCAAGCTGGACGAGGACAT 323
                                                                                                                                                                                                                       324 GAAGCGGCGCATCATCGCCCTAATCCTGGAGCGCCGTGAGCGCGCGACAAGGCGGCGGCGAT 383
                                                                                                                                                                                                                                                                                                                                                                                         244 caadecernaenteatricaturds de contrador d
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="AWB011.D10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CG 385
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
BE400165
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67 GCCGGACTGACCAAGAGCGAGTTGGCCAGGCGCATCCAGAAGG---ACCGGGCCACCGTC 123

Score 61.6; DB 10; Length 424; Pred. No. 23; 0; Mismatches 144; Indels 3

14.5%;

Conservative

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Similarity

Query Match Best Local S: Matches 161

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331 cechacenceladacricecchaderdericecesedricacentecedeceres 390
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on Aug 9 10:15:09 2004
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August 6, 2004, 08:50:04; Search time 156.122 Seconds (without alignments) 9439.175 Million cell updates/sec
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GenCore version 5.1.6
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1 cccggtacgggttcaattcccatcagtcacccg 34
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	972	0033	AX338975 Sequence	727	AY150032 Micromono	0 10	AY150028 Micromono	AY150029 Micromono	AX338973 Sequence	AX338977 Semience	AF481102 Candidatu	AY150030 Micromono	AX338976 Sequence	AF051097 Balanogio	U39716 Mycoplasma	AE000029 Mycoplasm	Continuation (5 of	AL139079 Campyloba	ACTORAGE MUSICE	AC112440 Rattus no	AC126653 Rattus no	AC094151 Rattus no	AF369748 Populus d	AC114820 Mus muscu	AC131173 Rattus no	ACI16514 Mus muscu	AC113251 Rattus no	AC107428 Rattus no	AC117974 Rattus no	AC004807 Mus muscu	ACCASOCA MUS MUSCU	AC102230 Mus muscu	AC026375 Mus muscu	AC108265 Rattus no	AC106669 Rattus no	AC110649 Rattus no	AC144875 Pongo pyg			DNA linear PAT 09-JAN-2002				sridae; Actinomycetales; ae; Micromonospora.	sa var africana pmlpl integrase	re-specific incegrat
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% Query e Match Length	4 100.0	4 100.0	4 100.0	4 100.0	3 97.1	4.77	73.5	5 73.5	73.5	0.67	72.4	70.6	70.6	4.0	ט עיני	62.6	65.9	.4 65.9 155932	0 V 0 V	65.3	65.3	64.7	64.1	64.1	64.1	64.1	4.0	62.9	62.9	62.4	4. 4	62.4	62.4	62.4	4.00	61.8	61.8			AX338972	T T C	AX338972.1 GI:1812	Micromonospora car Micromonospora car	Bacteria, Actinoba Micromonosporineae	Hosted, T.J. and Ho Isolation of Micro	and use or integra
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47 CCCCGGTACGGGTTCAATTCCCATCAGTCACCCG 80
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Micromonospora carbonacea
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Bacteriophage pMLP1
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Matches 34; Conservative
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Micromonospora halophitica and Micromonospora carbonacea chromosome Patent: WO 0187936-A 3 22-NOV-2001; SCHERING CORPORATION (US) Location/Qualifiers
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africana Waitz et al."
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Development of the Micromonospora carbonacea var. africana ATCC
39149 bacteriophage pMLP1 integrase for site-specific integration
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Hosted, T. Jr., Hewitt, D. D. and Alexander, D. C.
Direct Submission
Submitted (12-SEP-2002) New Lead Discovery, Schering-Plough
Research, 2015 Galloping Hill Road, Kenilworth, NJ 07033, USA
Location/Qualifiers
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Microbiology (Reading, Engl.) 149 (Pt 9), 2443-2453 (2003)
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1 (bases 1 to 145)
Alexander, D.C., Devlin, D.J., Hewitt, D.D., Horan, A.C. and
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                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="site of pSPRH840 recombination"
56. .79

    .34
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Micromonospora sp. ATCC 39149 attR region.
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Isolation of Micromonospora carbonacea var africana pmlp1 integrase and use of integrating function for site-specific integration into Micromonospora halophitica and Micromonospora carbonacea chromosome batent: WO 0187936-A 6 22-NOV-2001;
SCHERING CORPORATION (US)
  PAT 09-JAN-2002
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S Hosted, T.J. Jr., Alexander, D.C. and Hewitt, D.D.
Direct Submission.
In Submitted (12.5EP-2022) New Lead Discovery, Schering-Plough
Research, 2015 Galloping Hill Road, Kenilworth, NJ 07033, USA
Location/Qualifiers
1. 2025
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Microbiology (Reading, Engl.) 149 (Pt 9), 2443-2453 (2003)
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Alexander,D.C., Devlin,D.J., Hewitt,D.D., Horan,A.C. and
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Sequence 6 from Patent W00187936.
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/note="att/int region"
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AY150031
LOCUS
DEFINITION
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SOURCE
ORGANISM
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AUTHORS
TITLE
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VERSION
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AX338978
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/transl_table=11
/product == excisionase"
/product == excisionase"
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/db_xref="d1:2863042"
/db_xref="d2:2863042"
/db_xref="d
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PCSSTMLPRREPKEMKFLSDPEIGRLITALPPHWRPLVMLLVATGLRWGEAIGLRAGR
VDLLAARPRLTVVVGQLQELASTGELVPQSPKTAKGRRTVSFTTKVALLLTPLIAGKKS
                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAO46045.1"
| Ab_xref==G1:28630423"
| translation="MWIEKNGPVRIRDLVRGKKVTIQTGYPTKTSAKNAMVQFRAEQ
| LQGNALMPRGGOITADFVGFWWPSYEKTLKPTAVNSEGNRIRNHLLPILGHLTIDEL
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RRLGHSSIAVTDLLYGHLREEVDEGILAAIEEAMAGVRAEDLEAELDEELTDVLADAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Micromonospora nigra
Micromonospora nigra
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micromonosporineae; Micromonosporaceae; Micromonospora;
1 (bases 1 to 143)
Alexander, D. C., Devlin, D.J., Hewitt, D.D., Horan, A.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in Micromonospora spp
Microbiology (Reading, Engl.) 149 (Pt 9), 2443-2453 (2003)
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    .55
    /organism="Integration vector pSPRH840"

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Hosted,T.J. Jr., Hewitt,D.D. and Alexander,D.C.
Direct Submission
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Pred. No. 0.00016;
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/organism="Micromonospora nigra"
/mol_type="genomic DNA"
/strain="ATCC 33088"
/db_xref="ATCC;33088"
/db_xref="taxon:145857"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCCCGGTACGGGTTCAATTCCCATCAGTCACCCG 34
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1925. .1986
//note="attP element"
join(1969. .1986,1991. .2010)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 100.0%; Score 34; DB il Similarity 100.0%; Pred. No. 0.0 34; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                           codon_start=1
transl_table=11
                                                                                                                                                                                                          628. .1806
/gene="intM"
628. .1806
/gene="intM"
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Best Local Similarity
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misc_feature
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AY150032
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Isolation of Micromonospora carbonacea var africana pmlpl integrase and use of integrating function for site-specific integration into Micromonospora halophitica and Micromonospora carbonacea chromosome Patent: WO 0187936-A 9 22-NOV-2001; SCHERING CORPORATION (US) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-SEP-2003
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Bovelopment of the Micromonospora carbonacea var. africana ATCC
Dayl49 bacteriophage pMLP1 integrase for site-specific integration
in Micromonospora spp
Microbiology (Reading, Engl.) 149 (Pt 9), 2443-2453 (2003)
                                                                                                                                                                                                                                                                                                                         Gaps
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Micromonospora nigra
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Micromonosporineae, Micromonosporaceae, Micromonospora.
1 (bases 1 to 143)
Alexander, D.C., Devlin, D.J., Hewitt, D.D., Horan, A.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Micromonospora halophytica
Micromonospora halophytica
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micromonosporineae; Micromonosporaceae; Micromonospora.
                                                                                                                            /note="pSPRH840 attachment site; attB/attP identity
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100.0%; Pred. No. 0.00046;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Micromonospora halophytica"
/mol_type="unassigned DNA"
/db_xref="taxon:47864"
                                                                        'note="site of pSPRH840 recombination"
                                                                                                                                                                                                                                                                  Query Match 97.1%; Score 33; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 33; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ccccegracegerrcaarrcccarcagracec 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AX338978 260 bp
Sequence 9 from Patent WO0187936.
AX338978
                                                                                                                                                                                join(94. .105,110. .121)
1. .143
/note="attR region"
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/note="deposited in ATCC as Micromonospora carbonacea var. africana Waitz et al." africana Waitz et al." | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.145 | 1.1
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Bevelopment of the Micromonospora carbonacea var. africana ATCC
39149 bacteriophage pMLP1 integrase for site-specific integration
in Micromonospora spp
Microbiology (Reading, Engl.) 149 (Pt 9), 2443-2453 (2003)
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                           5..79
/note="tRNA-His"
/note="attachment site; attB/attP identity element"
join(85..98,103..116)
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Micromonospora sp. ATCC 39149
Bacteria, Actinobacteria, Actinobacteriae, Actinomycetales, Micromonosporineae, Micromonosporineae, Micromonosporaceae, Micromonosporaceae, Louss, Alexander 1 (bases 1 to 145)
Alexander D.C., Devlin, D.J., Hewitt, D.D., Horan, A.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56. .80
'note="pSPRH840 attachment site; attB/attP identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coases 1 to 145)
Hosted, T.J. Jr., Hewitt, D.D. and Alexander, D.C.
Direct Submission
Submitted M12-SEP-2002) New Lead Discovery, Schering-Plough
Research, 2015 Galloping Hill Road, Kenilworth, NJ 07033, US
Location/Qualifiers
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                                                                                                                                                                                                                                                                                         Length 145;
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/organism="Micromonospora sp. ATCC 39149"
/mol_type="genomic DNA"
/mol_type="ATCC 39149"
/db_xref="ATCC:39149"
/db_xref="ATCC:39149"
                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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/note="site of pSPRH840 recombination"
join(100. .117,122. .141)
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Micromonospora sp. ATCC 39149 attL region.
AY150029
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2.2;
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73.5%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 2.;
Matches 25; Conservative 0; Mismatches
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56..80
/note="attB region"
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VERSION
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PUBMED
REFERENCE
AUTHORS
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AY150029
LOCUS
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                               2 (bases 1 to 143)
Hosted, T.J. Jr., Hewitt, D.D. and Alexander, D.C.
Direct Submission
Submitted (12-SEP-2002) New Lead Discovery, Schering-Plough
Research, 2015 Galloping Hill Road, Kenilworth, NJ 07033, USA
Location/Qualifiers
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Hosted, T.J. Jr., Hewitt, D.D. and Alexander, D.C.
Direct Submission
Submitted (12.5EP-2002) New Lead Discovery, Schering-Plough
Research, 2015 Galloping Hill Road, Kenllworth, NJ 07033, USA
Location/Qualifiers
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/note="pSPRH840 attachment site; attB/attP identity
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Micromonospora sp. ATCC 39149
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Alexander, D.C., Devlin, D.J., Hewitt, D.D., Horan, A.C. and
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/organism="Integration vector pSPRH840"
/mol_type="genomic DNA"
/db_zref="taxon:219291"
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/note="site of pSPRH840 recombination"
join(100. .118,122. .138)
                                                                                                                                                                                                                                                             1.79
/organism="Micromonospora nigra"
/mol_type="genomic DNA"
/strain="ATCC 33088"
/db_xref="ATCC:33088"
/db_xref="taxon:145857"
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Micromonospora sp. ATCC 39149 attB region.
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/product="tRNA-His"
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AY150028.1 GI:28630424
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PAT 09-JAN-2002

DEFINITION ACCESSION VERSION

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AX338973

ORGANISM

KEYWORDS

AUTHORS TITLE

REFERENCE

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Candidatus Tremblaya princeps MviN (mviN) gene, partial cds, ribosomal protein L13 (rpL13), ribosomal protein S9 (rpS9), putative protein L13 (rpL13), ribosomal protein S9 (rpS9), putative protein H28 (hesB), dihydroxyacid dehydrase (ilvD), putative protein H28 (hesB), dihydroxyacid dehydrase (ilvD), s-enolpyruvylshikimate-3-phosphate synthase (arch), ribosomal protein L19 (rpL19), 5, 10-methylentetrahydrofolate reductase (merF), chaperone H59[0 (groE3), DNA polymerase alpha subunit (dnaE), valine sensitive acetolactate synthase III subunit (ilvI), ketol-acid reductoisomerase (ilvC), alpha-isopropylmalate synthase (levA), and ribosomal RNA, and SS ribosomal RNA, and Sybosomal RNA, and SS ribosomal RNA, and SS ribosomal RNA, and Sybosomal RNA, and SS ribosomal RNA, and SS ribosomal RNA, and SS ribosomal RNA, and SS ribosomal RNA, and sibosomal RNA, and SS ribosomal RNA, and sibosomal RNA, and ribosomal RNA, and sibosomal RNA, and unknown and some sibosomal RNA, and unknown
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Baumann,L., Thao,M.L., Hess,J.M. and Baumann,P.
Direct Submission
Submitted (06-FBB-2002) Microbiology, University of California, One Shields Ave., Davis, CA 95616-8665, USA
Location/Qualifiers
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Bacteria; Proteobacteria; Betaproteobacteria; Candidatus Tremblaya.

1 (bases 1 to 34806)
Baumann, L., Thao, M.L., Hess, J.M., Johnson, M.W. and Baumann, P.
The genetic properties of the primary endosymbionts of mealybugs differ from those of other endosymbionts of plant sap-sucking
                                                                                                                                                                                                                   Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Micromonosporineae, Micromonosporaceae, Micromonospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.5%; Score 25; DB 6; Length 315; 100.0%; Pred. No. 2.2; ive 0; Mismatches 0; Indels
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22083449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Micromonospora halophytica"
/mol_type="unassigned DNA"
/db xref="taxon:47864"
            DNA
Sequence 8 from Patent WO0187936.
AX338977
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Micromonospora halophytica
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                                                                                             AX338977.1 GI:18129113
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Best Local Similarity
Matches 25; Conserv
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolation of Micromonospora carbonacea var africana pmlp1 integrase and use of integrating function for site-specific integration into Micromonospora halophitica and Micromonospora carbonacea chromosome Patent: WO 018736.4 A 22-NOV-2001; SCHERING CORPORATION (US)
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micromonosporineae; Micromonosporaceae; Micromonospora.
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/mol_type="unassigned DNA"
/db xref="taxon:47853"
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/mol_type="unassigned DNA"
/db_xref="taxon:47853"
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Sequence 4 from Patent WO0187936
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Sequence 5 from Patent WO0187936
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100.0%; Pred. No.
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         56 GGGTTCAATTCCCATCAGTCACCCG
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Best Local Similarity
Matches 25; Conserv
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/translation="MLPQRASSAVRCCQGPMRSSRSSRCDKAAKCYFYTSSLRCMRHS
RRYASKPWACSMLAIRLRRCGARGRPAYQVVVADSRRKRNGVFLCRVGYYNPRLKSAH
IDTVMLRLWTERGAAPTRTVARLLHRHAAGCTAAARNSGSVCPHWQ"
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Chases 1 to 143)
Hosted,T.J. Jr., Hewitt,D.D. and Alexander,D.C.
Direct Submission
Submitted (12-SEP-2002) New Lead Discovery, Schering-Plough
Research, 2015 Galloping Hill Road, Kenilworth, NJ 07033, USA
Location/Qualifiers
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micromonosporinee; Micromonosporaceae; Micromonospora.
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/note="attachment site; attB/attP identity element"
join(94. .105,110. .121)
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Alexander,D.C., Devlin,D.J., Hewitt,D.D., Horan,A.C. and
Hosted,T.J.
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70.6%; Score 24; DB
Best Local Similarity 100.0%; Pred. No. 6.3
Matches 24; Conservative 0; Mismatches
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AY150030.
AX150030.1 GI:28630426
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56. .80
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          PAT 09-JAN-2002
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Micromonosporineae; Micromonosporaceae; Micromonospora.
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/mol_type="unassigned DNA"
/db_xref="taxon:47864"
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             DNA
Sequence 7 from Patent W00187936.
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Job time : 159.122 secs
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                                                                                                                               Micromonospora halophytica
Micromonospora halophytica
                                                                                                                                                                                                                                                          Hosted, T.J. and Horan, A.C.
                                                                                AX338976.1 GI:18129112
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6, 2004, 08:18:49; Search time 20.205 Seconds (without alignments) 7148.662 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 cccggtacgggttcaattcccatcagtcacccg 34
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                                                                                                                                                                                                                                                                                                      3373863 seqs, 2124099041 residues
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Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Post-processing:

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
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	Description	Aad25933	Aad25945	Aad25936	Aas08694	Aad25939 Micromono	Aad25934 Micromono	Aad25935	Aad25938 Micromono	Aad25937 Micromono	. 4	1	Abz26080	_	S Aaf15526 Thalassio	Ach26679 Human adu	C.	7 6 Continuation (7 of		Aaa6285	Aah24107 Human Per	Aak79597 Human imm	$^{\circ}$	mai mami imm
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The present invention relates to novel polymucleotides encoding integrase (int) and excisionase (xis) and an integrase attachment site (attP) which are isolated from pMLPI, a bacteriophage (lysogenic phage) isolated from Micromonospora carbonacea var. africana. Polymucleotides of the invention are useful for transforming an actinomycete with a vector. They are also useful for creating vectors for site-specific integration into host chromosomes. The integrating vectors are used to express actinomycete genes, manipulate secondary metabolic pathways and create new metabolic products such as hybrid antibiocics. The present sequence is pMLP1 attP site DNA from Micromonospora carbonacea Integrase; int; excisionase; xis; integrase attachment site; pMLP1; site-specific integration; hybrid antibiotic; metabolic product; secondary metabolic pathway; ds. Novel polynucleotides encoding integrase, excisionase and an integrase attachment site isolated from a lysogenic phage pMLP1, useful for transforming an actinomycete. Micromonospora carbonacea pMLP1 attP site DNA Claim 5; Page 33; 34pp; English. AAD25933 standard; DNA; 34 BP 15-MAY-2001; 2001WO-US015760. 17-MAY-2000; 2000US-0204670P. (first entry) Micromonospora carbonacea (SCHE ) SCHERING CORP. Hosted TJ, Horan AC; WPI; 2002-082983/11. WO200187936-A2. 26-MAR-2002 22-NOV-2001. AAD25933; AAD25933 

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Gaps

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Indels

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Integrase, int, excisionase, xis; integrase attachment site, attP, pMLP1, site-specific integration; hybrid antibiotic; metabolic product; secondary metabolic pathway; ds.
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                                         Length 34;
            Sequence 34 BP; 6 A; 14 C; 7 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_type= INVERTED
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167. .186
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                                                                                                                    CCCCGGTACGGGTTCAATTCCCATCAGTCACCCG 34
                                                                                                   CCCCGGTACGGGTTCAATTCCCATCAGTCACCCG 34
                                                                     0; Mismatches
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/note= "attP region"
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                      ch 100.0%;
1 Similarity 100.0%;
34; Conservative 0
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                                                                                                                                                                                                     AAD25945 standard; DNA; 209
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                                                                                                                                                                                                                                                                                                                                                                                Micromonospora carbonacea.
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                                        Query Match
Best Local Similarity
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Seguence 209 BP; 49 A; 64 C; 66 G; 30 T; 0 U; 0 Other;

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The present invention relates to novel polynucleotides encoding integrase (int) and excisionase (xis) and an integrase attachment site (attp) which are isolated from pMLP1, a bacteriophage (lysogenic phage) isolated from Micromonospora carbonacea var. africana. Polynucleotides of the invention are useful for transforming an actinomycete with a vector. They are also chromosomes. The integrating vectors for site-specific integration into host chromosomes. The integrating vectors are used to express actinomycete genes, manipulate secondary metabolic pathways and create new metabolic products such as hybrid antibiotics. The present sequence is pMLP1 attP/attB right juncture DNA from Micromonospora carbonacea
                                                                                                                                                                                                                                                                                  Integrase, int, excisionase, xis, integrase attachment site, attP, pMLP1, site-specific integration; hybrid antibiotic; metabolic product; attB, secondary metabolic pathway; attB/attP DNA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotides encoding integrase, excisionase and an integrase attachment site isolated from a lysogenic phage pMLP1, useful for transforming an actinomycete.
                                         Gaps
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0
                                                                                                                                                                                                                                                       Micromonospora carbonacea pMLP1 attP/attB right juncture DNA
          Length 209;
                                         Indels
          Score 34; DB 6; L
Pred. No. 2.5e-05;
; Mismatches 0;
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/note= "Inverted repeat 1 (IR1)"
148. .161
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                                                                                          CCCCGGTACGGGTTCATTCCCATCAGTCACCCG 125
                                                                    1 CCCCGGTACGGGTTCAATTCCCATCAGTCACCCG 34
100.0%; bcc.
100.0%; Pred. No. ...
0; Mismatches
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'note= "attP/attB region"
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/note= "Inverted repeat
complement(185. .247)
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                                                                                                                                                                      AAD25936 standard; DNA; 247
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/*tag= b
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                                         34; Conservative
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                           Similarity
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          Query Match
Best Local S:
Matches 34,
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                                                                                                                                      RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecules encoding everninomicin pathway gene products, useful for improving yields of everninomicin, to produce new everninomicin and as probes to identify homologous sequences.
                                                                                                                                                                                                                                                                                                         antibiotic; bottle-neck gene; orthomicin; fermentation;
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "Att/B/AttP region of integrase action"
                                                             .;
0
                                   Length 247;
                       Score 34; DB 6; Length 24
Pred. No. 2.6e-05;
       Sequence 247 BP; 38 A; 82 C; 90 G; 37 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= Insertion juncture
note= "Site of integrase activity"
                                                                                                              92 CCCCGGTACGGGTTCAATTCCCATCAGTCACCCG 125
                                                                                       1 CCCCGGTACGGGTTCAATTCCCATCAGTCACCCG 34
                                                                                                                                                                                                                                                                                  Micromonospora DNA encoding integrase enzymes.
                                  / Match 100.0%; Score 34; DB Local Similarity 100.0%; Pred. No. 2.6 nes 34; Conservative 0; Mismatches
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2570. .2799
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1394. .2572
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                     AAS08694 standard; DNA; 4388 BP
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                                                                                                                                                                                                                                                                                                                                                  sp. ATCC 39149.
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/*tag= d
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P-PSDB; AAU04900, AAU04912.
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useful for i
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Matches
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modified orsellinic acid groups contained in everninomicin, for expressing functional or mutant everninomicin biosynthetic enzyme for expressing functional or mutant everninomicin biosynthetic enzyme for explantion, diagnosis and preferably biosynthetis of everninomicins or other secondary metabolic products, improving the yield of everninomicins and to produce novel everninomicins and also as a hybridisation probe to can to produce novel everninomicins and also as a hybridisation probe to combinatorial biosynthesis to generate libraries of orthomycins, e.g. combinatorial biosynthesis to generate libraries of orthomycins, e.g. everninomicin analogues/homologues and drug discovery. The DNA encoding the integrase allows for increasing a given gene dosage. The integrate allows for increasing a given gene dosage. The integrate allows for increasing a given gene dosage. The integrate of choice into chromosomes of different hosts and to integrate genes of choice into chromosomes of different hosts and to integrate genes to vector can also be used to integrate antibiotic resistance genes in order to carry out bioconversions with compounds to which the strain is commanly sensitive and is thus useful in fermentation processes involving e.g. Streptomyces antibioticus. (Updated on 11-SEP-2003 to standardise OS field)
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modifications of the DNA sequence designed to change glycosyl and
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
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                                                                                                                                                                                                                                                                                                                                                     Sequence 4388 BP; 714 A; 1468 C; 1506 G; 694 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                          Length 4388;
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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155. .166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                34
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/note= "attP/attB region'
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26-MAR-2002
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RESULT 7
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                                                                                                                                 The present invention relates to novel polynucleotides encoding integrase (int) and excisionase (xis) and an integrase attachment site (attp) which are isolated from pMLPI. A bacteriophage (lysogenic phage) isolated from Micromonospora carbonacea var. Africana. Polynucleotides of the invention set useful for transforming an actinomycete with a vector. They are also useful for creating vectors for site-specific integration into host chromosomes. The integrating vectors are used to express actinomycete genes, manipulate secondary metabolic pathways and create new metabolic attp?AttB right juncture DNA from Micromonospora halophitica. (Updated on 07-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Integrase, int; excisionase, xis; integrase attachment site; attP; pMLP1; site-specific integration; hybrid antibiotic; metabolic product; attB; secondary metabolic pathway; ds.
                                                                   Novel polynucleotides encoding integrase, excisionase and an integrase attachment site isolated from a lysogenic phage pMLP1, useful for transforming an actinomycete.
                                                                                                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                                                                                                                               97.1%; Score 33; DB 6; Length 260; 100.0%; Pred. No. 7.2e-05;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                           Sequence 260 BP; 47 A; 83 C; 90 G; 40 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                             1 CCCCGGTACGGGTTCAATTCCCATCAGTCACCC 33
                                                                                                                                                                                                                                                                                                          larity 100.0%; Pred. No. 7.2
Conservative 0; Mismatches
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'note= "Inverted repeat 1
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/note= "Inverted repeat 2
complement(179. .241)
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/product= "attB peptide"
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/note= "tRNA-His DNA"
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/note= "attB region"
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                                                                                                               Claim 23; Fig 5; 34pp; English.
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          Hosted TJ, Horan AC;
                                 WPI; 2002-082983/11.
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les 33; Conserv
                                             P-PSDB; AAE15910
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The present invention relates to novel polynucleotides encoding integrase (int) and exclaionase (xis) and an integrase attachment site (attp) which are isolated from pWLP1, a bacteriophage (lysogenic phage) isolated from Micromonospora carbonacea var. africana. Polynucleotides of the invention are useful for transforming an actinomycete with a vector. They are also chromosomes. The integrating vectors are used to express actinomycete products such as hybrid antibolic pachways and create new metabolic products such as hybrid antibolics. The present sequence is pMLP1 attB DNA from Micromonospora carbonacea
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                                                                                                                                                                                                                           Novel polynucleotides encoding integrase, excisionase and an integrase attachment site isolated from a lysogenic phage pMLP1, useful for transforming an actinomycete.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 241 BP; 27 A; 78 C; 92 G; 44 T; 0 U; 0 Other;
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fnote= "Inverted repeat 1 (IR1)"
179. .198
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/note= "Inverted repeat 2 (IR2)"
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/*tag= b
/note= "attB/attP region"
157. .174
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62. .137
/*tag= a
/note= "tRNA-His DNA"
                                                                                                                                                                                                                                                                                                           Claim 23; Fig 4; 34pp; English
15-MAY-2001; 2001WO-US015760.
                                       17-MAY-2000; 2000US-0204670P.
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                                                                                  (SCHE ) SCHERING CORP
                                                                                                                         Hosted TJ, Horan AC;
                                                                                                                                                                WPI; 2002-082983/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Integrase; int; excisionase; xis; integrase attachment site; patfP; pMLP1; site-specific integration; hybrid antibiotic; metabolic product; attB; secondary metabolic pathway; attB/attP DNA; ds.
                                                                                                                                                                                             Novel polynucleotides encoding integrase, excisionase and an integrase attachment site isolated from a lysogenic phage pMLP1, useful for transforming an actinomycete.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 243 BP; 39 A; 74 C; 83 G; 47 T; 0 U; 0 Other;
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/note= "Inverted repeat 1 (IR1)"
162. .178
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/note= "Inverted repeat 2 (IR2)"
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/note= "attB/attP region"
140. .158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 GGTTCAATTCCCATCAGTCACCCG 137
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45. .120
/*tag= a
//note="LERNA-His DNA"
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                                                                                                                                                                                                                                                        Claim 23; Fig 4; 34pp; English.
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                                           15-MAY-2001; 2001WO-US015760
                                                                      17-MAY-2000; 2000US-0204670P
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26-MAR-2002
            22-NOV-2001
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15-MAY-2001; 2001WO-US015760 17-MAY-2000; 2000US-0204670P

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(SCHE ) SCHERING CORP Hosted TJ, Horan AC; WPI; 2002-082983/11.

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The present invention relates to novel polynucleotides encoding integrase (int) and excisionase (xis) and an integrase attachment site (attP) which are isolated from pMLPI, a bacteriophage (lysogenic phage) isolated from Micromonospora carbonacea var. africana. Polynucleotides of the invention are useful for transforming an actinomycete with a vector. They are also useful for creating vectors for site-specific integration into host chromosomes. The integration octors are used to express actinomycete genes, manipulate secondary metabolic pathways and create new metabolic attBAattP left juncture DNA from Micromonospora halphilica. (Updated on 07-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                             Novel polynucleotides encoding integrase, excisionase and an integrase attachment site isolated from a lysogenic phage pMLP1, useful for transforming an actinomycete.
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/note="Inverted repeat 1 (IR1)"
150. .161
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/*tag= b
/note= "attB region"
134. .145
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/*tag= a
/note= "tRNA-His DNA"
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(first entry)
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26-MAR-2002
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Mouse, DNase X, apoptosis, systemic lupus erythematosus, cystic fibrosis, acquired immune deficiency syndrome; AIDS, cancer, prostatic atrophy, transgenic, dermatological, immunosuppressive, antiinflammatory, anti-HIV; cytostatic, gene, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention iseful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB77071). The sequence data for this partent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                     Drosophila melanogaster expressed polynucleotide SEQ ID NO 30914.
                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5546 BP; 1398 A; 1240 C; 1213 G; 1695 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 30914; 21pp + Sequence Listing; English.
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85.2%; Pred. No. 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 TACGGGTTCAATTCCCATCAGTCACCC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABZ26080 standard; DNA; 40116 BP
ABL12144/c
ID ABL12144 standard; cDNA; 5546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li PWD,
                                                                                                                                                                                                                                                                                                                                        23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical; gene; ss.
                                                                                                                                                                                                                            Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
P-PSDB; ABB68041.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                   WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interactions.
                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                     27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAR-2003
                                                            ABL12144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABZ26080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
ABZ26080/c
                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ttinuaTion (5 of 6) of AAT58840 from base 400001 (Mycoplasma genitalium genome. )
Sequence split into 6 fragments LOCUS AAT58840 Accession Aat58840
Fragment Name Begin End
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel polynucleotides encoding integrase (int) and excisionase (xis) and an integrase attachment site (attp) which are isolated from pMLP1, a bacteriophage [1ysogenic phage] isolated from Micromonospora carbonacea var. africana. Polynucleotides of the invention are useful for transforming an actinomycete with a vector. They are also useful for creating vectors for site-specific integration into host chromosomes. The integrating vectors are used to express actinomycete products such as hybrid antibiotics. The present sequence is PMLP1 attB DNA from Micromonospora halophytica. (Updated on 07-AUG-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotides encoding integrase, excisionase and an integrase attachment site isolated from a lysogenic phage pMLP1, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
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Pred. No. 0.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 255 BP; 33 A; 78 C; 94 G; 50 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                       /rpt_type= INVERTED
/note= "Inverted repeat 2 (IR2)"
complement(191..253)
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Pred. No. 12;
0; Mismatches
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                                                                                /*tag= e
/product= "attB peptide"
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310000
410000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGTTCAATTCCCATCAGTCACCC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 GGGTTCAATTCCCATCAGTCACCC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 23; Fig 5; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        transforming an actinomycete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.9%;
                                                                                                                                                                                                            15-MAY-2001; 2001WO-US015760.
                                                                                                                                                                                                                                               17-MAY-2000; 2000US-0204670P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.68;
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200001
300001
400001
500001
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       /*tag=
                                                                                                                                                                                                                                                                                     (SCHE ) SCHERING CORP
                                                                                                                                                                                                                                                                                                                        Hosted TJ, Horan AC;
                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-082983/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATS8840 4
Continuation (5 of 6) of WP Sequence split into 6 WP AATS8840 0 WP AATS8840 1 WP AATS8840 2 WP AATS8840 3 WP AATS8840 3 WP AATS8840 4 WP AATS8840 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAE15910
                                                                                                                                     WO200187936-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  field.)
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Gaps

.. O

Matches

à g RESULT 11

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and related vectors, proteins and diseases that involve apoptosis, e.g.

The invention relates to a DNA (I) that: (i) (ABZ26077-ABZ26079) encodes any of three splice forms of murine DNasax (II) of 295, 295 and 61 amino acids (ABS604013-ABS60405); (ii) is a 40116 bp genomic sequence (ABZ26080) (i or (iii) encodes a protein (IIa) with the biological properties of (II) and is a fragment or allelic or other variant of (i) or (ii). DNase X cogrates DNA inducing apoptocis, immunogenic DNA complexes inhibiting the immune response in systemic lupus erythematosus and mucus in the lungs of cystic fibrosis patients. (I), vectors containing (I) and the encoded proteins (II), are used to diagnose, prevent or treat diseases associated (with apoptosis, specifically systemic lupus erythematosus, acquired immune deficiency syndrome, cancer, cystic fibrosis and prostatic carrophy. Also (I) and (I) can be used to screen for specific binding carrophy. Also (I) and (I) can be used to screen for specific binding carrophy. Also (I) and (I) can be used to screen for specific binding cleared (particularly inactivated) are used to study the specified diseases and/or to characterise genes and/or for testing potential characterises genes and/or for testing potential control of the invention

Sequence 40116 BP; 11523 A; 9280 C; 9062 G; 10251 T; 0 U; 0 Other;

0; 60.0%; Score 20.4; DB 7; Length 40116; 95.5%; Pred. No. 78; ive 0; Mismatches 1; Indels 0; Query Match
Best Local Similarity 95.5.
These 21; Conservative

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à g RESULT 13 

AAF15421 standard; DNA; 348 BP

AAF15421,

09-MAR-2001 (first entry)

Thalassiosira weissflogii plastid ssrA gene, SEQ ID NO:167.

ssrA gene; tmRNA; bacterium; chloroplast; diatom; detection; detection; identification; quantification; characterisation; nucleic acid array; DNA chip; drug design; treatment monitoring; contamination; ds.

Thalassiosira weissflogii

WO200070086-A1.

23-NOV-2000

15-MAY-2000; 2000WO-IE000066

99WO-IE000043 14-MAY-1999;

ssrA gene, tmRNA, or fragments of them, as target regions in probe for detection of prokaryotic or eukaryotic organisms, and for compositions of the invention have applications in medicine, and also in industry (e.g., for assessing bacterial contamination of a foodstuff or an environmental sample). Sequences AAF15338-F15442 represent ssrA genes, or fragments thereof, from a wide variety of organisms ENTERPRISE IRELAND T/A BIORESEARCH IRELA. UNIV NAT IRELAND GALWAY. Claim 26; Page 82-83; 221pp; English assays for detection of p determination of species. Smith TJ; WFI; 2001-025025/03 Barry TG, (IRBI-) (UYNA-) Use of 

Sequence 348 BP; 124 A; 47 C; 49 G; 128 T; 0 U; 0 Other;

Gaps 0 DB 5; Length 348; Indels 57.6%; Score 19.6; Dl 84.6%; Pred. No. 77; iive 0; Mismatches Conservative Query Match Best Local Similarity Matches 22; Conserv

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8 ACGGGTTCAATTCCCATCAGTCACCC 33

a ò

RESULT 14
AAF15526
ID AAF15
XX
AC AAF15
XX
DT 09-MA

AAF15526 standard; RNA; 348 BP

AAF15526;

(first entry) 09-MAR-2001

us-09-855-340a-3.rng

321 ATGGGTTCAATTCCCATCAGTTCCAC 346

WO200070086-AL 14-MAY-1999; 23-NOV-2000. Barry TG, (IRBI-) (UYNA-) Use of 

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Query Match
Best Local Similarity 84.6%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                  ACH26679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DRMA/)
(LABA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DICK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (STAC/)
                                                                                                                                                                                                                             RESULT 15
ACH26679/c
                                                                                                                                                g
                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contraction relates to the safe give of themse, an and lead of casts gone, or fragments thereof as target regions in a nucleic acid probe assay for the detection and identification of prokaryotic and/or cukaryotic organisms. The invention also relates to 38 novel sara cukaryotic organisms. The invention also relates to 38 novel sara compared to probe and probe as target region in chloroplasts and characterial, genus- and species specific sara gene/thanka-directed probes and profession in the same and is also found in chloroplasts and diatoms. It has a dual function both as a tRNA and as a mRNA and is involved in rescuing truncated mRNAs which have lost stop codons. Sara genes and the as a transpect regions in nucleic acid probe assays for the detection, identification, or quantification of a prokaryotic or cukaryotic organism. CDNA transcripts of thank molecules may also be used as a target region in a nucleic acid hybridisation assays. A fragment of the sara gene or a tmRNA molecule corresponding to a region of high homology from the 5' and or the 3' and of the DNA molecule can be used as a target region in a nucleic acid probe assay, while a fragment of the sara gene or a tmRNA molecule corresponding to a region of the mology can be used as a target region to distinguish between specific or distinguishing between living and dead prokaryotic or eukaryotic organisms, and in a multiple probe format for broad scale detection and or distinguishing between living and dead prokaryotic organisms. A fragment of the target regions may be used as the basis of an assay for dentification of prokaryotic or eukaryotic organisms, and in a multiple probe can be linked to a microarray gene or distinguishing between living and dead prokaryotic organisms. A fragment of the target regions may be used to moline and or the the target regions may be used as the basis of an assay of dentification of prokaryotic or eukaryotic organisms. A fragment of the target regions and distinguishing and distinguishing and distinguishing and dista
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   efficacy of drug therapies against infectious agents. Target regions may also be used to monitor the viability and level of problotic organisms in the gastrointestinal tract. The methods and nucleic acids and compositions of the invention have applications in medicine, and also in industry (e.g., for assessing bacterial contamination of a foodstuff or an environmental sample) Sequences AAF15443-F15547 represent tmRNAs, or fragments thereof, from a wide variety of organisms
                                        ssrA gene; tmRNA; bacterium; chloroplast; diatom; detection; detection; identification; quantification; characterisation; nucleic acid array; DNA chip; drug design; treatment monitoring; contamination; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ssrA gene, tmRNA, or fragments of them, as target regions in for detection of prokaryotic or eukaryotic organisms, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an RNA transcript
Thalassiosira weissflogii plastid tmRNA, SEQ ID NO:168
                                                                                                                                                                                                                                                                                                                                                                                                              BIORESEARCH IRELA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to the ssrA gene or tmRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; Page 83; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         ENTERPRISE IRELAND T/A B UNIV NAT IRELAND GALWAY.
                                                                                                                                                                                                                                                                                                            LS-MAY-2000; 2000WO-IE000066.
                                                                                                                                                                                                                                                                                                                                                             99WO-IE000043
                                                                                                                                                      Thalassiosira weissflogii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    determination of species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith TJ;
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (SGT) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The purified polypeptide is one of the 38043 isolated obNA/SSI sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formet directly from 19770 at
                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
                                                                 Gaps
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      Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jones
                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 438 BP; 150 A; 73 C; 81 G; 131 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dickson MC,
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      ņ,
      DB
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; Pred. No. 80;
0; Mismatches
Score 19.6; |
Pred. No. 77;
                                                                 6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 13891; 44pp; English.
                                                                                                                                                            321 AUGGGUUCAAUUCCCAUCAGUUCCAC 346
                                                                                                                            33
                                                                                                                            8 ACGGGTTCAATTCCCATCAGTCACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUL-2001; 2001US-00918995.
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                                                                                                                                                                                                                                                                                                                                                ACH26679 standard; cDNA; 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human adult ovary cDNA #5059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
Query Match
Best Local Similarity 61.5
Matches 16; Conservative
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DICKSON M C.
JONES L W.
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LABAT I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-615964/58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-OCT-2003
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Gaps

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4; Indels

Sequence 348 BP; 124 A; 47 C; 49 G; 0 T; 128 U; 0 Other;

DB

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Search completed: August 6, 2004, 09:47:34 Job time: 23.205 secs

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APPLICANT: WATANABE, HIDEMI
APPLICANT: HATORI, MASAHIRA
APPLICANT: SARAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REPERBENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR APPLICATION NUMBER: JP2000-107160
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN US: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Appli
Sequence 892, App
Sequence 7, Appli
Sequence 2, Appli
                                                                                  August 6, 2004, 09:31:14; Search time 4.08664 Seconds (without alignments) 4617.079 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 32
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Sequence 1
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Sequence 6
Sequence 7
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Sequence 1
Sequence 5
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Sequence 1
Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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3 US-09-103-840A-1

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US-09-489-039A-359
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US-08-815-1175-2
US-07-925-695-6
US-07-925-695-7
US-08-307-444A-10
US-08-587-389-10
US-09-023-655-1326
US-09-023-655-1326
US-09-023-655-137
US-08-757-659A-17
US-08-757-659A-17
US-08-757-659A-17
US-08-757-659A-17
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US-09-088-337B-23
PCT-US93-11153-23
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US-09-548-938A-9
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US-09-790-988-1
US-09-134-000C-892
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                                                                                                                                                                                                                                                 682709 seqs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        - nucleic search, using sw model
                                                                                                                                                                                                        IDENTITY NUC Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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9511
9511
22463
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                                                                                                                                              Title:
Perfect score:
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No.
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	71 71 71 71 71		2213 2213 2213 252	ব ব ব ব ব ব ব	-09-489-039A-4623 -09-489-039A-4636 -09-489-039A-5524 -09-489-039A-6553 -09-409-039A-6556	4 4 8 9 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	
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O 45	17.	ιΛ 	2904	4	5-35 MENT	Sequence 3, Appli	
RESULT 1 US-08-545-528D-1; Sequence 1, Ap.; Parent No. 653; GENERAL INFORM; APPLICANT: FT.; ITILE OF INVE	SULT 1 -08-545-528 Sequence 1, Patent No. GENERAL INC. APPLICANT: TITLE OF I	plicati 7773 ATION: aser et	on US/0854!	,085	545528D de Sequence of the Mycoplasma	Genitalium Genome,	Fragment
PATENT I TITLE ( PILLE R. CURREN CURREN PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR ) SEQ ID ) LENGTH	TITLE OF O. TITLE OF O. FILE REFER CURRENT AP CURRENT APPL PRIOR FILI PRIOR FILI PRIOR FILI NUMBER OF SOFTWARE: SOFTWARE: EQ ID OL	PITTE OF INVENTION: Thereof, and FILE REFERENCE: PB193P1 CURRENT FAPILICATION NUMBER: US/08/ CURRENT FILING DATE: 1995-10-19 PRIOR APPLICATION NUMBER: US 08/48 PRIOR FILING DATE: 1995-06-07 PRIOR FILING DATE: 1995-06-07 PRIOR FILING DATE: 1995-06-07 NUMBER OF SEQ ID NOS: 1 SSGTWARE? PATENELL NOS: 1 SSGTWARE? PATENELL VETSION 3.1	Thereof, an 3P1 19P1 19P3 1995-10-19 MBER: US 08/ 995-06-07 1995-06-07 1: 1	t: U US US US US C-07	, and Uses Thereof 08/88545,528D 019 08/488,018 7 08/473,545		
; TYPE: ; ORGAN US-08-545 Query M Best Lo Matches	TYPE: DNA ORGANISM: My -08-545-528D-1 Query Match Best Local Sim Matches 23;	TYPE: DNA ORGANISM: Mycoplasma geni 8-545-528D-1 6-5. st Local Similarity 95. tches 23; Conservative	ge acije	mital 15.9%; 15.8%;	lium ; Score 22.4; DB 4; Length ; Pred. No. 2.5; 0; Mismatches 1; Indel	1 580073; s 0; Gaps 0	
& €	10	O GGGTTCAATTC            8 GGGTTCAATTC	TCCCAT	8=8	CAGTCACCC 33           CAGTCGCCC 445151		
RESULT 2 US-09-790-988-1/C ; Sequence 1, App ; Patent No. 6632 ; GENERAL INFORMA ; APPLICANT: SHI	2 90-988 nce 1, it No. AL INF ICANT:	SULT 2 -09-790-988-1/c Sequence 1, Application US/09790988 Parent No. 6632935 GENERAL INFORMATION: APPLICANT: SHIGENOBU, SHUJI APPLICANT: WATANABE, HIDEMI	on US/09	760, IN:	790988		

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Gaps
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; Sequence 256, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
    APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES:
    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                         Sequence 2, Application US/08815175
Patent No. 5856139
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
ITLE OF INVENTION: NOVEL PROLINE-RICH ACIDIC PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
  Indels
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                                        2 CCCGGTACGGGTTCAATTCCCATCAGTCACCCG 34
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Pred. No. 18;
0; Mismatches
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,175
FILING DATE: Filed Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Billings, Lucy J. RECISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
TELEPHONE: 415-855-0555
TELEFRAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: Filed Herewit
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 69.7%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      596 base pairs
  24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY: PANCTUT02
CLONE: 2235738
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STATE: C
COUNTRY:
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US-08-815-175-2
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  Matches
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APPLICANT: Oblsen, Kari
APPLICANT: Oblsen, Kari
APPLICANT: Oblsen, Kari
APPLICANT: Oblsen, Kari
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERET
FILE REFERENCE: ELITRA.008A
CURRENT APPLICATION NUMBER: US/09/711,164
CURRENT FILING DATE: 1090-11-09
PRIOR APPLICATION NUMBER: US 60/164415
PRIOR FILING DATE: 1999-11-9
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                       ;
0
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US-09-134-000C-892/c
Sequence 892, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BYDEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-08-15
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                                                                                                                              Length 640681;
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                                                                                                                                                                         Indels
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                                                                                                                                DB 4;
                                                                                                                              Query Match 57.6%; Score 19.6; D
Best Local Similarity 84.6%; Pred. No. 51;
Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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56.5%; Score 19.2;
Best Local Similarity 87.5%; Pred. No. 9.6
Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                  -8 ACGGGTTCAATTCCCATCAGTCACCC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 GGGTTCGATTCCCATCGGTCGCCC 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09711164
Patent No. 6589738
GENERAL INFORMATION:
APPLICANT: Forsyth, R. Allyn
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)...(839)
OTHER INFORMATION: n = A, T, C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Escherichia coli
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                                          TYPE: DNA
ORGANISM: Buchnera sp.
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Best Local Similarity
SEQ ID NO 1
LENGTH: 640681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 7
LENGTH: 839
                                                                                     US-09-790-988-1
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55.3%; Score 18.8; D
66.7%; Pred. No. 39;
tive 3; Mismatches
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                                                                                                                                                                                                                    FILING DATE: 19920807
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 287402/91
FILING DATE: 09-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 360441/91
FILING DATE: 05-DEC-1991
ATTONNEY, AGBNI TINORMATION:
NAME: Weilacher, Robert G.
REGISTRATION NUMBER: 20,531
REFERENCE/DOCKET NUMBER: 06/87-48009
TELECHONEN: (202) 659-2811
TELEFAX: (202) 659-2811
TELEFAX: WUI 64470
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 9511 Dec.
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9511 base pairs
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Best Local Similarity 66.77
Matches 20; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
CITY: Washington STATE: D.C.
                                                          20036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-925-695-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-925-695-7
                                         COUNTRY:
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Patent No. 5428145

GENERAL INFORMATION:
APPLICANT: OKAMOTO, Hiroaki
APPLICANT: NAKAMOTA, Tetsuo
TITLE OF INVENTION: NON-B HEPATITIS VIRUS GENOME,
TITLE OF INVENTION: DOLYNUCLEOTIDES, POLYPEPTIDES, ANTIG
TITLE OF INVENTION: DETECTION SYSTEMS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beveridge, Degrandi, Weilacher & Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Beveridge, DeGrandi, Weilacher & Young
1850 M Street, N.W., Suite 800
                                                                         COMPUTER: Diskette
COMPUTER: IBN Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FactSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2051 cegnacaraticertraccarcactesce 2022
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Best Local Similarity 76.7%; Pred. No. 35;
Matches 23; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                 PRICK APPLICATION DATA:

APPLICATION NUMBER: PP1162
FILING DATE: 31-DBC-1997
RICK APPLICATION DATA:

APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRICK APPLICATION DATA:

APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRICK APPLICATION NUMBER: PC7/AU98/01023
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 273
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-494-0792
  STREET: 755 PAGE MILL ROAD CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS:
LENGTH: 6305 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 1...6305
                                                              COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
US-09-221-017B-256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -07-925-695-6
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Sequence 7, Application US/07925695
Fequence 7, Application US/07925695
Fequence 7, Application US/07925695
Federal INFORMATION:
APPLICANT: OKAMOTO, Hiroaki
APPLICANT: NAKAMURA, Tetsuo
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, ANTIGEN, ANTIBODY AND
TITLE OF INVENTION: DETECTION SYSTEMS
TITLE OF INVENTION: DETECTION SYSTEMS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beveridge, DeGrandi, Weilacher & Young
STREET: 1850 M Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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ZIP: 20036
COMPUTER: 20036
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TRM PC COMPASIBLE
COMPUTER: PATEMIN PC COMPASIBLE
COMPUTER: PATEMIN PC DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/925,695
PTITING DATE: 19920807
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/925,695
FILING DATE: 19920807
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Sequence 10, Application US/08307444A Patent No. 5516659
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-307-444A-10
         US-08-307-444A-10
                                                                                                                                                                                                                                                                                                 CITY: ALL
STATE: VI
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-08-587-389-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9

US-09-644-460-28/C

Sequence 28, Application US/09644460

Patent No. 6657053

GENERAL INFORMATION:
APPLICANT: Fisher, Paul B.
TITLE OF INVENTION: Display
FILE REFERENCE: 34587-C-PCT-USA
CURRENT FILING DATE: 2000-08-23

PRIOR PILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: PCT/US99/04323

PRIOR PILING DATE: 1999-02-26

PRIOR PILING DATE: 1998-11-03

PRIOR PILING DATE: 1998-11-03

PRIOR FILING DATE: 1998-02-27

NUMBER OF SEC ID NOS: 42

SOFTWARE: FastSEQ for Windows Version 4.0

SEC ID NO 28

LANDER OF SEC ID NOS: 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18.6; DB Pred. No. 29; 0; Mismatches
FILING DATE: 09-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 36041/91
FILING DATE: 05-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: RAFLICATION NUMBER: 20.53
REFERENCE/DOCKET NUMBER: 06/87-48009
TELECOMMUNICATION INFORMATION:
TELEPAN: (202) 659-2811
TELEPAN: (202) 659-2811
TELEPEX: WUI 64470
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LEMOTH: 9511 base pairs
TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CCCGGTACGGGTTCAATTCCCATCAGTCAC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.3%; Score 18.8; 76.7%; Pred. No. 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: unsure
CCATION: 652, 1523
COTHER INFORMATION: c, t, a or g;
NAME/KEY: misc_feature
LOCATION: (1)...(1538)
COTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 72.7%;
Matches 24; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 76.7
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-925-695-7
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RESULT 10

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PREMIRAL NO. 551(58)

PREMIRAL NO. 551(58)

PREDICANT: WILL ANSWER

PREDICANT: WAS ANDRESSES: WAS AN
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Fatent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Coffrey J. Sellhamer
ITILE OF INVENTION: EXPRESSION
VUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET 3174 PORTER DRIVE
CITY: PALO ALTO
COTATE CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                           Gaps
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  Length 3466;
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                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
Score 18.6; DB 4;
Pred. No. 36;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
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                                                                                                                                   2450 cccassartissccaacticaccisastraccic 2482
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                                                                                          1 CCCCGGTACGGGTTCAATTCCCATCAGTCACCC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 72.7%; Pred. No. 37;
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIPICATION:
ATTORNEY FAGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REPERRENCE/DOCKET NUMBER: PA-0001 US
TELECOMMINICATION INFORMATION:
TELECHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/08770379; Patent No. 2844564; GENERAL INFORMATION:
APPLICANT: Chang, Yuan
  Query Match
Best Local Similarity 72.7%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3653 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , CLONE: 9339656
US-09-023-655-1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: lin
IMMEDIATE SOURCE
LIBRARY: GENB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-08-770-379-17/c
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Sequence 1, Application US/09880484D

Patent No. 6632791

GENERAL INFORMATION:
APPLICANT: Light, David
APPLICANT: Nagashima, Mariko
APPLICANT: Machael J

TITLE OF INVENTION: Thrombomodulin Analogs for Pharmaceutical Use
FILE REPERENCE: 51863AUSM1

CURRENT APPLICATION NUMBER: US/09/880,484D

CURRENT FILING DATE: 2001-06-12

PRIOR FILING DATE: 2000-06-21

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin version 3:1

SEQ ID NO 1

TYPE: DAA

TYPE: DAA

TYPE: DAA

TYPE: DAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2463;
                                                                                     COMPUTER REALDE FORM:

COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BE PLOPPY disk
COMPUTER: BEACHIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/587,389
FILING DATE: U-JAN-1996
CLASSIPICATION 1435
PRING APPLICATION NUMBER: US/08/587,444
ATFORNEY/AGENT INPORMATION:
NAME: OLIFF, JAMES A:
REGISTRATION NUMBER: 27,075
REBERENCE/DOCKET NUMBER: 27,075
REBERENCE/DOCKET NUMBER: 27,075
REBERENCE/DOCKET NUMBER: 27,075
TELEPAK: (703) 836-6400
TELEPAK: (703) 836-2787
TELEPAK: (703) 836-2787
TELEEX: 90-1799 PTO ALEX
SEQUENCE CHARACTER/STICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.7%; Score 18.6; DB 1; 72.7%; Pred. No. 33; tive 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2338 cccaedaacredeccaacricacricaercacec 2370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CCCCGGTACGGGTTCAATTCCCATCAGTCACCC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 72.7
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2463 bases
TYPE: nucleic acid
STRANDEDNESS: single
                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (151)..(1875)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: mat peptide LOCATION: (205)..()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION:
US-09-880-484D-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ANTI-SENSE: NO
US-08-587-389-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-09-880-484D-1
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FEATURE:

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                                                             APPLICANT: Moore, Patrick S.

TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
CORRESPONDENCE: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chang, Yuan
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Relamn, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                           STATE: New YORK

ZIP: 10036
COUNTRY: 10036
COMPUTER READBLE FORM:
MEDIUW TYPE: FIDEPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
FILING DATE:
CLASSIFICATION: 435
ATTONERY/AGENT INFORMATION:
NAME: White: John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
TELEPPAN: (212) 278-0400
TELEPPAN: (212) 278-0400
TELEPPAN: (212) 391-0525
INFORMATION FOR SEQ ID NO: 17:
SEGUENCE CHRARACTERISTICS:
LENTH: 3510 Dase Pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURE: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7143 cccassraccscrashracccrickscrrccc 7111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 72.7%; Pred. No. 69;
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-08-757-669A-17/c
'Sequence 17, Application US/08757669A
'Patent No. 6183751
Bohenzky, Roy A.
Russo, James J.
Edelman, Isidore S.
Moore, Patrick S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: DNA (genomic)
US-08-770-379-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 1005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid strandEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper &
                                                                                                                                                                                      STREET: 1185 A.C. CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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62.9 496 14 CD221929 14 62.9 617 28 BZ253996 14 62.9 619 14 CD228161 15 62.4 512 28 AZ663671 15 62.4 647 28 BH698487 15 62.4 647 28 AZ663662 16 61.2 369 28 AZ662876 16 61.2 369 29 CG962621	3 61.2 459 28 B2Z55997 3 61.2 481 28 B2866799 3 61.2 503 12 B1128480 3 61.2 772 28 BZ440539 3 61.2 772 28 CC335988 5 61.2 777 29 CG95642 5 61.2 842 29 CG926738 6 61.2 846 29 CG932119	61.2 881 28 BZ405594 61.2 882 12 BT736662 8 61.2 896 29 CG953021 8 61.2 931 29 CG953021 8 61.2 1161 12 BG342311 5 60.6 499 29 TA134G07Q 5 60.6 589 28 AQ272293 6 60.6 589 9 AV3785146 4 60.0 274 9 AV338955	20.4         60.0         478         10         BE654144         BE654144         BE654144         LPM-ANI-200.90           20.4         60.0         640         10         BE634824         BE634824         UV85C04.x           20.4         60.0         654         10         BE484517         BE634824         UV85C04.x           20.4         60.0         659         14         CB441703         CB441703         ML5E-2276           20.4         60.0         779         13         BU562772         BU562772         AGENCOURT           20.4         60.0         966         9 AV327597         AV327597         AV327597         AV327597           20.4         60.0         1890         11         AX031860         AX031860         MLS muscu           20.4         60.0         2893         11         AX031867         AX037906         MLS muscu           20.2         60.0         3747         11         AX037906         AX037906         MLS muscu           20.2         59.4         247         12         B1003984         RC4-HN004           20.2         59.4         338         9         AA343504         AX3343504         BZ4245283	ALIGNMENTS AZ933974 689 bp DNA lir BJ_Ba0001H19r B. japonicum BAC library Brady; genomic, genomic survey sequence.	ON A2933974  A2933974.1 GI:13776034  S GS. Bradyrhizobium japonicum ISM Bradyrhizobium japonicum Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium.  E Dases I to 689; Tomkins,J.P., Wood,T.C., Stacey,M.G., Loh,J.T., Judd,A., Golcoechaa,J.L., Stacey,G., Sadowsky,M.J. and Wing,R.A.  A marker-dense, sequence-ready map of the Bradyrhizobium japonicum	NAL Genome Res. 11 (8), 1434-1440 (2001)  INE 21376150  MED 1483585  T Contact: Wing RA  Clemson University  IOU Jordan Hall, Clemson, SC 29634, USA  Tel: 864 656 7288  Fax: 864 656 4293  Email: rwing@clemson.edu
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5.1.6 Compugen Ltd. search time 131.685 Seconds	(without alignments) 7710.163 Million cell updates/sec agtcacccg 34	ues :s: 55026578			results predicted by chance to have a	Description  A2933974 BJ Ba000  BF165844 60174875  B7883122 AGENCOURT  BF540384 602050148
GenCore version 5.1 Copyright (c) 1993 - 2004 Comp OM nucleic - nucleic search, using sw model Run on: Auqust 6, 2004, 09:22:34 ; Searc	(without a tritle: US-09-855-340A-3 Ferfect score: 3 decoggtacgggttcaattcccatcagtcaccg Scoring table: IDENTITY_NUC Gapop 10.0, Gapox 1.0	89 segs, 1493: atisfying cho: 0 200000000 num Match 100% num Match 100%	Feet 1	12: gb est3:* 13: gb_est4:* 14: gb est5:* 15: em_estfun:* 16: em_eston:* 17: em_gss_hum:* 19: em_gss_liv:* 20: em_gss_vrt:* 21: em_gss_pln:*	22: em_gss_mam:* 23: em_gss_mam:* 24: em_gss_mrs:* 25: em_gss_rod:* 26: em_gss_rod:* 27: em_gss_vrl:* 27: em_gss_vrl:* 28: gb_gss_r* 29: gb_gss2:* No. is the number of results	g derived by analysis of the SUMM SUMM SUMM STAND B ID STAND SUMM STAND

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Homo sapiens (human)
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26; Conservative
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BF540384
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/note="Organ: lung; Vector: pCWV-SPORT6; Site 1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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/strain="czech II"
/db xref="ltaxon:10090"
/clone="IMAGE:3995514"
/tissue type="spontaneous tumor, metastatic to mammary.
/lab_host="pH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 689;
                                                                                                                                                                                                                                              db_xref="taxon:375"
|lab_host==E.coli"
|clone lib="B. japonicum BAC library"
|note="Vector: pindigo536; Site_1: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                    /organism="Bradyrhizobium japonicum"
/mol_type="genomic DNA"
/strain="USDA110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.9%; Score 22.4; DB 28; ilarity 81.2%; Pred. No. 1.36+02; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        639 CCCTGTGCCGGTTCAATTCCCGTCGGCC 608
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Class: BAC ends
High quality sequence stop: 636.
Location/Qualifiers
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Gaps

614 ccccedinacacincharitrocorcadiorocci 646

1 CCCCGGTACGGGTTCAATTCCCATCAGTCACCC 33

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/ussue type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab.host="bH10B."
/clone lib="Lubski dorsal root ganglion"
/clone lib="Colored lib="Colo
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
BQ889122
AGENCOURT 8113048 Lupski_dorsal_root_ganglion Homo sapiens cDNA
clone IMAGE:6178968 5', mRNA sequence.
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Email: cgapbs-romail.nih.gov
Trissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llh.gov
Plate: LLAMN3559 row: g column: 01
High quality sequence stop: 500.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:6178968"
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BQ889122.1 GI:22281136
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BF540384.1 GI:11627765
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us-09-855-340a-3.rst

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BZ253996.1 GI:23957934
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Enbryophyta; Paccae;

Eukarota; Viridiplantae; Andropogoneae; Sorghum.

E 1 (bases 1 to 456)

S Cordonnier-Pratt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S.,

Klein,R.R., Liang,C., Sun,F., Sullivan,R., Shah,M., Rathore,K.,

Eastman,A. and Pratt,L.H.

An EST (database from Sorghum: callus culture and cell suspension

Unpublished (2003)

Other_ESTS: CCC1 1 E04.91_A007

Other_ESTS: Ccc1 1 E04.91_A007

Other_ESTS: Ccc1 2 E04.91_A007

Contactory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tal: 706 583 0210

Email: mmpratteuga.edu

Therm: Annowerstenda.edu

Therm: Annowerstenda.edu
                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol type="mRNA"
/stain="FVB/N"
/db_xref="rexon:10090"
/clone="IMAGE:4189667"
/lab_host="DHIOB (IT phage-resistant)"
/clone lib="NLC GAps SG2"
/note="Organ: salivary gland; Vector: pGNV-SPORT6; Site 1:
Not; Site_2: Sali; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1:3 kb. Constructed by Life
Technologies. Note: this is a NCI_GGAP Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       496 bp mRNA linear EST 21-MAY-2003 CCC1 1 E04.b1 A007 Callus culture/cell suspension Sorghum bicolor CD521929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science, plant material and RNA prepared at Texas A & W University, sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 64.1%; Score 21.8; DB 10; Best Local Similarity 78.8%; Pred. No. 2.4e+02; Matches 26; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         602 CCCCGGTACCCCTACAATTTTCCCTCAGTCTCCC 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCCCGGTACGGGTTCAATTCCCATCAGTCACCC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sorghum bicolor (sorghum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD221929.1 GI:30965363
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CD221929/c
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AUTHORS
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The following services of the following services services of the following services services of the following services s
                                                                                                                                                                                                                     /organism="Sorghum bicolor"
/mol_type="mRNA"
/mol_type="mRNA"
/culcivar="RT430"
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/dlone="CCC1 1 E04 A007"
/dlone lib="Callus culture/cell suspension"
/dlone lib="Callus culture/cell suspension"
/done lib="Reflex"
/done lib="suspensed from a mixture of polyar RNA from callus culture tissue and cells in suspension culture.
Double-stranded cDNA was cloned unidirectionally into different Draili site is CACTGTGTG, 3-prime Dralli site is CACTGTGTG, 3-prime Dralli site is CACCATGTG, 3-prime Dralli site is CACCATGTG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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80.6%; Pred. No. 3.2e+02;
ative 0; Mismatches 6.
exclude polyA.
Seg primer: Sug3 (CGACCTGCAGCTCGAGCACA)
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255 CCCGCACAGGTTCGATTCCCATCCTTCACCC 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Norway rat)
                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           location/Qualifiers
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80.68;

Best Local Similarity

/cell\_type="Brain" /clone\_lib="CHOR1-230 Segment 2" /nore="Wector: pTARBAC1.3; Site\_1: MboI; Site\_2: MboI; CHOR1-230 Rat (BN/SsNHsd/MCW) BAC library produced by

sex="Female"

Pieter de Jong"

; 0

Gaps . 0 617;

Length Indels

Score 21.4; DB 28; Pred. No. 3.3e+02;

62.9%; 80.6%;

Query Match Best Local Similarity

0; Mismatches

25; Conservative

Matches

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9 10:16:09 2004

Mon Aug

/db.xref="rexactive for the following property of the following for the following following for the following foll

Query Match

(http://www.jax.org/resource/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant valouity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pMAD42 (gril #472114|gpl AF12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xili0-Gold (Stratagene) cells and selected for ampicillin resistance." DB 28; Length 512; 62.4%; Score 21.2; Query Match

Wis musculus (house mouse)
Wis musculus
Bukarya: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukarya: Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 512)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Niederhausern, A. and Wright, D., Weise, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weise, R.
Mouse, whole genome scaffolding with paired end reads from 10kb AZ663671 1058 14-DEC-200 DNA linear GSS 14-DEC-200 1M0543K22F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0543K22 F, genomic survey sequence. /sex="Male"
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/clone lib="Mouse lokb plasmid UUGCIM library"
/note="Wetcr: PWD42ry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, Laboratory Mouse DNA Resource 382 CCCGCACAGGTTCGATTCCCATCCTTCACCC 352 1. .512 /organism="Mus musculus" /mol type="genomic DNA" /strain="C57BL/6J" /db xref="taxon:10090" /clone="UUGCIM0543K22" 3 CCGGTACGGGTTCAATTCCCATCAGTCACCC AZ663671 AZ663671.1 GI:11800817 plasmid inserts Unpublished (2000)

B

Gaps ; 0 Pred. No. 3.3e+02; 0; Mismatches 6; 33 25; Conservative source DEFINITION ORGANISM REFERENCE AUTHORS Matches ACCESSION VERSION KEYWORDS SOURCE JOURNAL RESULT 8 AZ663671 FEATURES TITLE COMMENT ઠે 셤

Sorghum bicolor Sorghumn, Sorghumn Strong Sorghum bicolor Sorghum bicolor Spermatophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

E 1 (Dases 1 to 619)

Cordonier-Patt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S., Klein,R.R., Liang,C., Sun,F., Sullivan,R., Shah,M., Rathore,K., Eastman,A. and Pratt,L.H.

An EST database from Sorghum: callus culture and cell suspension Unpublished (2003)

Other ESTs: CCC1 6 C06.91\_A007

Contact: CordonTer-Pratt PM

Laboratory for Genomics and Bicinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 583 0210

TITLE JOURNAL COMMENT

AUTHORS REFERENCE

CCCI\_6 C06.bl\_A007 Callus culture/cell suspension Sorghum bicolor cDNA clone CCCI\_6 C06\_A007 3', mRNA sequence.
CD228161

Sorghum bicolor (sorghum)

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

CD228161/c DEFINITION CD228161.1 GI:30971595

Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & W University,
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude poly.

Seg primer: Sug3 (CGACCTGCAGCTCGAGCACA)
POLYA=No.

Location/Qualifiers

source

FEATURES

/organism="Sorghum bicolor" /mol\_type="mRNA" /cultivar="RTx430"

5

LOCUS

RESULT 9 BH698487

g

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

AUTHORS TITLE JOURNAL COMMENT

REFERENCE

us-09-855-340a-3.rst

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwDA2 (gilfyla) A1219/[A] A1220/2.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chamically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
      Mouse ...
plasmid inserts
plasmid inserts
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Fel: 801 585 506
Fax: 801 585 7177
Email: ddunnagenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0543 row: I column: 24
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 649.
I. 649
..... musculus"
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R., Tingey, A., von
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="Mouse 10kb plasmid UUGCiM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 62.4%; Score 21.2; DB 28; Length 649; Best Local Similarity 88.5%; Pred. No. 4e+02; Matches 23; Conservative 0; Mismatches 3; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 GTACGGGTTCAATTCCCATCAGTCAC 31
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Mus musculus
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         TITLE
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                                                                                                                                                                                                                                                                                             BH698487 BO 2 3 KB Brassica oleracea genomic clone BOHXM56, genomic survey sequence.
BH698487.1 GI:18772681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brassica oleracea
Brassica oleracea
Brassica oleracea
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Oupublished (2001)
Other GSS: BOHXM56TF
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Mus musculus
Mus musculus
Mus musculus
Mus resea, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 649)
Dunn,D., Acyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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-clone="BOHXMS6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
                                     Indels
      Pred. No. 3.9e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Brassica oleracea"
                                                                                                                        299 GAACTGGTTCAATTCCCAGCAGTCAC 324
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                                                                                      6 GTACGGGTTCAATTCCCATCAGTCAC 31
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GSS.
Best Local Similarity 88.5%;
Matches 23; Conservative
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FEATURES

ORIGIN

0;

AZ663662 LOCUS DEFINITION

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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS

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/clone lib="mth2"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Cook, D.R. and Kim, D.J, unpublished"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 425;
                                                                                         9712 Medical Center Drive, Rockville, MD 20850, USA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.2%; Score 20.8; DB 29;
llarity 78.1%; Pred. No. 5.5e+02;
Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                        /organism="Medicago truncatula"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CCCGGTACGGGTTCAATTCCCATCAGTCACCC 33
                                                                                                                                                                                                                                                                                         /mol type="genomic DNA"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="47D16"
                                                                                                              Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
Seg primer: CAGGAAACAGCTATGACC
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Zea mays"
                                                                                                                                                                                                              Location/Qualifiers
1. .425
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Location/Qualifiers
1. .459
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Unpublished (2003)
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seg primer: TF
                   Other GSSs: MBBFX20TF
Contact: Chris Town
TIGR
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches 25, Conserva
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Best Local Similarity
Matches 25; Conserv
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Zea mays
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BZ755997
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymorlectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. Coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CG962621 425 bp DNA linear GSS 15-DEC-2003
MBEFX20TR mth2 Medicago truncatula genomic clone 47D16, genomic
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Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                        plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UDCCIM library."
/note="Wector: PWG4Zuv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
    whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Town, C.D., Shetty, J., Koo, H. and Feldblyum, T.F.
Sequencing of BAC ends from Medicago truncatula
                                                                                                                                                                 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                       Insert Length: 10000 Std Error: (Plate: 0534 row. H column: 08 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 369.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0534H08"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  survey sequence.
CG962621
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84112, USA
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Best Local S:
Matches 22
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CG962621/c
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PUPBL38TD ZM 0.6_1.0 KB Zea mays genomic clone ZMMBTa281G04,
genomic survey sequence.
BZ755997.1 GI:28908378
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /molltype="genomic DNA"
/strain="B73"
/db xref="taxon:4577"
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COT selected genomic DNA library"
                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermartophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
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6, 2004, 13:39:06
  BI128480.1 GI:18012435
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Best Local Similarity
---hes 25; Conserva
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Job time : 135.685 secs
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AUTHORS
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Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

712 Medical Center Dr., Rockville, MD 20850, USA

721: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the bovine BAC library CHORI-240

(http://www.chori.org/Dacpac/boxine240.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/Dacpac/ordering information.htm). This work

was undertaken as part of the International Bovine BAC Mapping

Consortium (IBBMC) by AgResearch Ltd., New Zealand and The

Institute of Genomic Research (TIGR), USA.

Seg primer: T7

Seg primer: T7

Class: BAC ends.
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                                                                                                                                              481 bp DNA linear GSS 18-MAR-2003 CH240_287E17.TV CHORI-240 Bos taurus genomic clone CH240_287E17, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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/clone_lib="CHORI-240"
/note="Vector: pTARBAGL.3; Site_l: Mbol; Site_2: Mbol;
Hereford bull il Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 481)
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
Shvartsbeyn,A., Gebregeorgis,E., Chen,D., Riggs,F., de Jong,P.,
Crawford,A.M. and McEwan,J.C.
Bovine BAC End Sequences from Library CHORI-240
Unpublished (2003)
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                                               145 CCATGCGCGTGTTCAATTCCCATCATTCAACC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCCCGGTACGGGTTCAATTCCCATCAGTCACC 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="CH240_287E17"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Populus tremula x Populus tremuloides

SM Populus tremula x Populus tremuloides

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.

E (bases 1 to 503)

Hitonen, T., Karlsson, J., Teeri, T., Gustáfsson, P., Bahlerao, R., Jansson, S., Nilsson, O., Sundberg, B., Nilsson, P., Uhlen, M., Gene expression in Populus

Unpublished (2001)

Contact Erlandsson R.
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/mol type="mRNA"
/db_xref="taxon:4764"
/clone lib="Populus cambium cDNA library"
/note="Organ: cambium"
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                                                                                                                                                                                                                                                                                                                                                           Department of Biotechnology
Royal Institute of Technology
Teknikringen 30, Stockholm S-10044, Sweden
Tel: 46 8 790 8287
Eax: 46 8 245452
Email: rikerl@biochem.kth.se.
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